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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 05:24:18 ; Search time 2566.56 Seconds  
(without alignments)  
11346.531 Million cell updates/sec

Title: US-09-497-957-9\_COPY\_465\_1065

Perfect score: 601

Sequence: 1 CAGATGTGCTGCAGCTGAG.....GGAAGAGCAGACATATACGT 601

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:.\*  
1: gb\_ba:.\*  
2: gb\_htg:.\*  
3: gb\_in:.\*  
4: gb\_om:.\*  
5: gb\_ov:.\*  
6: gb\_pat:.\*  
7: gb\_ph:.\*  
8: gb\_pl:.\*  
9: gb\_pr:.\*  
10: gb\_ro:.\*  
11: gb\_sts:.\*  
12: gb\_sy:.\*  
13: gb\_un:.\*  
14: gb\_vi:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	601	100.0	860	9 AY205604	AY205604 Homo sapi
2	601	100.0	1200	9 AF115265	AF115265 Homo sapi
3	601	100.0	1280	9 HSA249335	AJ249335 Homo sapi
4	601	100.0	1317	6 AX407339	AX407339 Sequence
5	601	100.0	1440	6 AR117793	AR117793 Sequence
6	601	100.0	1440	6 AR117794	AR117794 Sequence
7	601	100.0	1440	6 AR117795	AR117795 Sequence
8	601	100.0	1440	6 AR117796	AR117796 Sequence
9	601	100.0	1440	6 AR149463	AR149463 Sequence
10	601	100.0	1440	6 AR149464	AR149464 Sequence
11	601	100.0	1440	6 AR149465	AR149465 Sequence
12	601	100.0	1440	6 AR149466	AR149466 Sequence
13	601	100.0	2506	6 AR199238	AR199238 Sequence
14	601	100.0	2506	6 AR275757	AR275757 Sequence
15	601	100.0	2716	6 CO17466	CO17466 Sequence
16	601	100.0	2727	9 HSU50319	U60319 Homo sapien
17	533	88.7	1123	9 BC074721	BC074721 Homo sapi
18	507	84.4	1045	9 AF079407	AF079407 Homo sapi
19	504.4	83.9	823	9 AF079408	AF079408 Homo sapi

20	504.4	83.9	1085	9 HSA249336	AJ249336 Homo sapi
21	486.8	81.0	686	9 AF144240	AF144240 Homo sapi
22	484.2	80.6	1320	4 AY007541	AY007541 Ceratopthe
23	481	80.0	1319	4 AY007544	AY007544 Rhinocero
24	481	80.0	1320	4 AY007543	AY007543 Dicerorhi
25	477.8	79.5	2332	4 AY007542	AY007542 Dicerorhi
26	410.4	68.3	781	9 AF079409	AF079409 Homo sapi
27	377	62.7	789	10 AF008587	AF008587 Rattus no
28	377	62.7	1706	10 RNERHAEM	AJ001517 Rattus no
29	377	62.7	3520	10 BC070942	BC070942 Rattus no
30	357.4	59.5	1529	10 MM066849	U66849 Mus musculu
31	337.4	56.1	819	10 AF176534	AF176534 Rattus no
32	320.4	53.3	492	9 AF144241	AF144241 Homo sapi
33	286.6	47.7	489	9 AF144239	AF144239 Homo sapi
34	277	46.1	874	9 HSHLAH2	Y09800 H. sapiens H
35	277	46.1	5982	6 AX701831	AX701831 Sequence
36	277	46.1	10825	6 AR117789	AR117789 Sequence
37	277	46.1	10825	6 AR117790	AR117790 Sequence
38	277	46.1	10825	6 AR117791	AR117791 Sequence
39	277	46.1	10825	6 AR117792	AR117792 Sequence
40	277	46.1	10825	6 AR149459	AR149459 Sequence
41	277	46.1	10825	6 AR149460	AR149460 Sequence
42	277	46.1	10825	6 AR149461	AR149461 Sequence
43	277	46.1	10825	6 AR149462	AR149462 Sequence
44	277	46.1	11214	9 AF447807	AF447807 Pan trogl
45	277	46.1	12146	6 AR199263	AR199263 Sequence

#### ALIGNMENTS

RESULT 1	AY205604	860 bp	mRNA	linear	PRI 03-MAR-2003
LOCUS	AY205604	Homo sapiens hemochromatosis (HFE)	mRNA	partial cds.	
DEFINITION	AY205604				
ACCESSION	AY205604.1	GI:28800981			
VERSION					
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 860)				
AUTHORS	Kutlar,F., Nechtman,J. and Leithner,C.				
TITLE	Direct isolation of hemochromatosis (HFE) mRNA from the whole blood of a normal Caucasian individual				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 860)				
AUTHORS	Kutlar,F., Nechtman,J. and Leithner,C.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-DEC-2002) Medicine/Hematology-Oncology/Hemoglobin DNA Laboratory, Medical College of Georgia, 15th Street, Laney Walker, AC-1000, Augusta, GA 30912, USA				

#### FEATURES

source	1..860	/organism="Homo sapiens"
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PSPSGTLVIGVISGIAVFAVVILLFIIILRRQSGRGAMGHVLAERE"

ORIGIN	Query Match		100.0%;	Score 601;	DB 9;	Length 860;	
	Best Local Similarity		100.0%;	Pred. No. 3.2e-160;			
	Matches	601;	Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
QY	1	CAGATGTGGCTGCAGCTGAGTTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC	60				
Db	5	CAGATGTGGCTGCAGCTGAGTTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC	64				
QY	61	TTCTGGACTATTATGGAATAATCAACACACAGCAGAGGATGCCACACCTCGCAGGTCATC	120				
Db	65	TTCTGGACTATTATGGAATAATCAACACACAGCAGAGGATGCCACACCTCGCAGGTCATC	124				
QY	121	CTGGGCTGTGAATGCAAGAAGCAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT	180				
Db	125	CTGGGCTGTGAATGCAAGAAGCAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT	184				
QY	181	GGCAGGACCACTTGAATTTCTGCCCTGCACACTGGATTGGAGAGCAGCAGAACCCAGG	240				
Db	185	GGCAGGACCACTTGAATTTCTGCCCTGCACACTGGATTGGAGAGCAGCAGAACCCAGG	244				
QY	241	GCTGSCCCACCAAGCTGGAGTGGGAAGCACAAGATTTCGGGCCAGGCAGACAGGGCC	300				
Db	245	GCTGSCCCACCAAGCTGGAGTGGGAAGCACAAGATTTCGGGCCAGGCAGACAGGGCC	304				
QY	301	TACTTGGAGGAGTGCCTCTGCACAGCTGCAGCAGTGTCTGGAGCTGGGGAGGTGTT	360				
Db	305	TACTTGGAGGAGTGCCTCTGCACAGCTGCAGCAGTGTCTGGAGCTGGGGAGGTGTT	364				
QY	361	TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTTCAGTGACC	420				
Db	365	TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTTCAGTGACC	424				
QY	421	ACTCTAGGTGTGCGGCTTGAATACTACTACCCCAAGCAATCATCATGAGTGGCTGAAG	480				
Db	425	ACTCTAGGTGTGCGGCTTGAATACTACTACCCCAAGCAATCATCATGAGTGGCTGAAG	484				
QY	481	GATAAGCAGCAATGATGCAAGGATTCGAACCTTAAAGACCTATTGGCCCAATGGGAT	540				
Db	485	GATAAGCAGCAATGATGCAAGGATTCGAACCTTAAAGACCTATTGGCCCAATGGGAT	544				
QY	541	GGGACCTACAGGGCTGGATAACCTTTGGCTGTATACCCCTGGGGAAGCAGAGATATACG	600				
Db	545	GGGACCTACAGGGCTGGATAACCTTTGGCTGTATACCCCTGGGGAAGCAGAGATATACG	604				
QY	601	T 601					
Db	605	T 605					

RESULT 2	AF115265	1200 bp	mRNA	linear	PRI 07-MAY-2001
LOCUS	Homo sapiens hemochromatosis termination variant tere6 (HFE) mRNA, complete cds.				
DEFINITION	Homo sapiens hemochromatosis termination variant tere6 (HFE) mRNA, complete cds.				
ACCESSION	AF115265				
VERSION	AF115265.1	GI:11094314			
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Thenie,A., Orhant,M., Gicquel,I., Fergelot,P., Le Gall,J.Y., David,V. and Mosser,J.				
TITLE	The HFE gene undergoes alternate splicing processes				
JOURNAL	Blood Cells Mol. Dis. 26 (2), 155-162 (2000)				
MEDLINE	20448010				
PUBMED	11001625				
REFERENCE	2 (bases 1 to 1200)				

AUTHORS	Thenie A., Orhant, M. and Mosser, J.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-DEC-1998) UPR 41 CNRS, Faculte de Medecine, 2, av du Pr. Bernard, Rennes 35043, France		
FEATURES	Location/Qualifiers		
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ORIGIN			
	Query Match	100.0%;	Score 601; DB 9; Length 1200;
	Best Local Similarity	100.0%;	Pred. No. 3.3e-160;
	Matches	601; Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	CAGATGTGGCTGCAGTGCAGTCTGAAAGGGTGGGATCACATGTTCTACTGTTGAC	60
Db	255	CAGATGTGGCTGCAGTGCAGTCTGAAAGGGTGGGATCACATGTTCTACTGTTGAC	314
QY	61	TTCTGGACTATTATGGAAATCACAAACACAGCAGAGGAGTCCACACCTCGCAGGTCATC	120
Db	315	TTCTGGACTATTATGGAAATCACAAACACAGCAGAGGAGTCCACACCTCGCAGGTCATC	374
QY	121	CTGGGCTGTGAAATGCAAGAAGCAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT	180
Db	375	CTGGGCTGTGAAATGCAAGAAGCAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT	434
QY	181	GGCAGGACCACTTGAATTTGCGCTGCACACTGGAATTGGAGAGCAGACAGACCCAGG	240
Db	435	GGCAGGACCACTTGAATTTGCGCTGCACACTGGAATTGGAGAGCAGACAGACCCAGG	494
QY	241	GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAGACAGGGCC	300
Db	495	GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAGACAGGGCC	554
QY	301	TACCTGGAGAGGAGTGCCTCTGCACAGCTGCAGCAGTGTCTGGAGCTGGGGAGAGGTGT	360
Db	555	TACCTGGAGAGGAGTGCCTCTGCACAGCTGCAGCAGTGTCTGGAGCTGGGGAGAGGTGT	614
QY	361	TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACC	420
Db	615	TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACC	674
QY	421	ACTCTACGGTGTGGGCTTGAATACTACCCCAAGACATCACCATGAAGTGGCTGAAG	480
Db	675	ACTCTACGGTGTGGGCTTGAATACTACCCCAAGACATCACCATGAAGTGGCTGAAG	734
QY	481	GATAAGCAGCAATGGATGCCAAGGAGTTCGAACCTTAAAGACGTTATGGCCCAATGGGGAT	540
Db	735	GATAAGCAGCAATGGATGCCAAGGAGTTCGAACCTTAAAGACGTTATGGCCCAATGGGGAT	794
QY	541	GGGACCTACAGGGCTGGATAACCTTGGCTGTATACCCCTGGGGAAGCAGAGATATACG	600
Db	795	GGGACCTACAGGGCTGGATAACCTTGGCTGTATACCCCTGGGGAAGCAGAGATATACG	854
QY	601	T	601



Db 855 T 855

RESULT 3  
HSA249335 1280 bp mRNA linear PRI 02-JUL-2004  
LOCUS Homo sapiens mRNA for hemochromatosis protein (HFE gene) splice  
DEFINITION variant 1.  
ACCESSION AJ249335  
VERSION AJ249335.1 GI:15485418  
KEYWORDS alternative splicing; hemochromatosis protein; HFE gene.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Sanchez, M., Bruguera, M., Rodas, J. and Oliva, R.  
TITLE Complete characterization of the 3' region of the human and mouse hereditary hemochromatosis HFE gene and detection of novel splicing forms  
JOURNAL Blood Cells Mol. Dis. 27 (1), 35-43 (2001)  
MEDLINE 21257661  
PUBMED 11358357

REFERENCE  
AUTHORS Oliva, R.  
TITLE Direct Submission  
JOURNAL Submitted (06-SEP-1999) Oliva R., Faculty of Medicine and Clinic Hospital, Human Genome Research Group, Casanova 143, 08036, SPAIN

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ORIGIN  
Query Match 100.0%; Score 601; DB 9; Length 1280;  
Best Local Similarity 100.0%; Pred. No. 3.3e-160;  
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGATGTGGCTGAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTGAC 60  
DB 335 CAGATGTGGCTGAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTGAC 394  
QY 61 TTCTGACTATTATGAAATATCAACACAGCAAGAGTCCACACCCCTGCAGGTCAATC 120  
DB 395 TTCTGACTATTATGAAATATCAACACAGCAAGAGTCCACACCCCTGCAGGTCAATC 454  
QY 121 CTGGGCTGTGAATGCAAGAGCAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180  
DB 455 CTGGGCTGTGAATGCAAGAGCAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 514

QY 181 GGCAGGACCACTTGAATTTGCTCCCTGACACACTGGATTGGAGCAGCAGAACCCAGG 240  
DB 515 GGCAGGACCACTTGAATTTGCTCCCTGACACACTGGATTGGAGCAGCAGAACCCAGG 574  
QY 241 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAACAAGATTCCGGCCAGGCAAGAGGCC 300  
DB 575 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAACAAGATTCCGGCCAGGCAAGAGGCC 634  
QY 301 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTGTGCTGGAGTGGGGAGAGGTGT 360  
DB 635 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTGTGCTGGAGTGGGGAGAGGTGT 694  
QY 361 TTGGACCAACAAGTGGCTCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCACTGACC 420  
DB 695 TTGGACCAACAAGTGGCTCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCACTGACC 754  
QY 421 ACTTACCGGTGTCGGGCTTGAACCTACTACCCCAAGAACATCACCATTGAAGTGGCTGAAG 480  
DB 755 ACTTACCGGTGTCGGGCTTGAACCTACTACCCCAAGAACATCACCATTGAAGTGGCTGAAG 814  
QY 481 GATAAGCGCAATGATGCCAGAGGTTTCGAACCTAAAGACGTTATTCGCCAATGGGAT 540  
DB 815 GATAAGCGCAATGATGCCAGAGGTTTCGAACCTAAAGACGTTATTCGCCAATGGGAT 874  
QY 541 GGCAGCTTACCGGCTGGGATAACCTTGGCTGTACCCCTCGGGAAGAGCAGAGATATACG 600  
DB 875 GGCAGCTTACCGGCTGGGATAACCTTGGCTGTACCCCTCGGGAAGAGCAGAGATATACG 934  
QY 601 T 601  
DB 935 T 935

RESULT 4  
AX407339 1317 bp DNA linear PAT 14-JUN-2002  
LOCUS Sequence 1 from Patent WO0224929.  
DEFINITION AX407339  
ACCESSION AX407339  
VERSION AX407339.1 GI:21440046  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Ehrlich, R., Rotem-Yehudar, R. and Laham, N.  
TITLE A soluble beta 2 microglobulin (betazm)/hfe monochain for biotechnological and therapeutic applications  
JOURNAL Patent: WO 0224929-A 1 28-MAR-2002;  
Ramat University Authority for Applied Research & Industrial Dev LTD. (II)

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ORIGIN



Query Match	100.0%;	Score 601;	DB 6;	Length 1317;	
Best Local Similarity	100.0%;	Pred. No. 3.3e-160;			
Matches 601;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	CAGATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC	60		
DB	580	CAGATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC	639		
QY	61	TTCTGGACTATTATGGAATCAACACAGCAAGGAGTCCACACCCCTGCAGGTCATC	120		
DB	640	TTCTGGACTATTATGGAATCAACACAGCAAGGAGTCCACACCCCTGCAGGTCATC	699		
QY	121	CTGGGCTGTGAATGCAAGAGACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT	180		
DB	700	CTGGGCTGTGAATGCAAGAGACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT	759		
QY	181	GGGACGACACCTTGAATTCGCTGACACACTGGATTGGAGAGCAGACAGCCAGG	240		
DB	760	GGGACGACACCTTGAATTCGCTGACACACTGGATTGGAGAGCAGACAGCCAGG	819		
QY	241	GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCACAAGATTTCGGGCCAGGAGCC	300		
DB	820	GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCACAAGATTTCGGGCCAGGAGCC	879		
QY	301	TACCTGGAGGAGTGCCTTGCACAGCTGCAGAGTTCGAGAGTGGGGAGAGTGT	360		
DB	880	TACCTGGAGGAGTGCCTTGCACAGCTGCAGAGTTCGAGAGTGGGGAGAGTGT	939		
QY	361	TTGGACCAACAGTGCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC	420		
DB	940	TTGGACCAACAGTGCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC	999		
QY	421	ACTCTACGCTGTCGGGCTTGAACCTACTACCCCAAGAGTTCGAACCTTTCAGTGAAG	480		
DB	1000	ACTCTACGCTGTCGGGCTTGAACCTACTACCCCAAGAGTTCGAACCTTTCAGTGAAG	1059		
QY	481	GATAACAGCAATGATGCAAGAGTTCGAACCTTTCAGTGAAGTGGGAT	540		
DB	1060	GATAACAGCAATGATGCAAGAGTTCGAACCTTTCAGTGAAGTGGGAT	1119		
QY	541	GGGACCTACAGGCTGGATACCTTGGCTGTACCTTGGCTGGGAGAGCAGATATACG	600		
DB	1120	GGGACCTACAGGCTGGATACCTTGGCTGTACCTTGGCTGGGAGAGCAGATATACG	1179		
QY	601	T 601			
DB	1180	T 1180			
RESULT 5					
LOCUS	AR117793	1440 bp	DNA	linear	PAT 16-MAY-2001
DEFINITION	Sequence 9 from patent US 6140305.				
ACCESSION	AR117793				
VERSION	AR117793.1	GI:14098699			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1440)				
AUTHORS	Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D., Tsuchihashi,Z. and Wolff,R.K.				
TITLE	Hereditary hemochromatosis gene products				
JOURNAL	Patent: US 6140305-A 9 31-OCT-2000;				
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source	1..1440				
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ORIGIN					
Query Match	100.0%;	Score 601;	DB 6;	Length 1440;	
Best Local Similarity	100.0%;	Pred. No. 3.4e-160;			
Matches 601;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	

QY	1	CAGATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC	60		
DB	465	CAGATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC	524		
QY	61	TTCTGGACTATTATGGAATCAACACAGCAAGGAGTCCACACCCCTGCAGGTCATC	120		
DB	525	TTCTGGACTATTATGGAATCAACACAGCAAGGAGTCCACACCCCTGCAGGTCATC	584		
QY	121	CTGGGCTGTGAATCAAGAGACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT	180		
DB	585	CTGGGCTGTGAATCAAGAGACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT	644		
QY	181	GGGACGACACCTTGAATTCGCTGACACACTGGATTGGAGAGCAGACAGCCAGG	240		
DB	645	GGGACGACACCTTGAATTCGCTGACACACTGGATTGGAGAGCAGACAGCCAGG	704		
QY	241	GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCACAAGATTTCGGGCCAGGAGCC	300		
DB	705	GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCACAAGATTTCGGGCCAGGAGCC	764		
QY	301	TACCTGGAGGAGTGCCTTGCACAGCTGCAGAGTTCGAGAGTGGGGAGAGTGT	360		
DB	765	TACCTGGAGGAGTGCCTTGCACAGCTGCAGAGTTCGAGAGTGGGGAGAGTGT	824		
QY	361	TTGGACCAACAGTGCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC	420		
DB	825	TTGGACCAACAGTGCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC	884		
QY	421	ACTCTACGCTGTCGGGCTTGAACCTACTACCCCAAGAGTTCGAACCTTTCAGTGAAG	480		
DB	885	ACTCTACGCTGTCGGGCTTGAACCTACTACCCCAAGAGTTCGAACCTTTCAGTGAAG	944		
QY	481	GATAACAGCAATGATGCAAGAGTTCGAACCTTTCAGTGAAGTGGGAT	540		
DB	945	GATAACAGCAATGATGCAAGAGTTCGAACCTTTCAGTGAAGTGGGAT	1004		
QY	541	GGGACCTACAGGCTGGATACCTTGGCTGTACCTTGGCTGGGAGAGCAGATATACG	600		
DB	1005	GGGACCTACAGGCTGGATACCTTGGCTGTACCTTGGCTGGGAGAGCAGATATACG	1064		
QY	601	T 601			
DB	1065	T 1065			
RESULT 6					
LOCUS	AR117794	1440 bp	DNA	linear	PAT 16-MAY-2001
DEFINITION	Sequence 10 from patent US 6140305.				
ACCESSION	AR117794				
VERSION	AR117794.1	GI:14098700			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1440)				
AUTHORS	Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D., Tsuchihashi,Z. and Wolff,R.K.				
TITLE	Hereditary hemochromatosis gene products				
JOURNAL	Patent: US 6140305-A 10 31-OCT-2000;				
FEATURES	Location/Qualifiers				
source	1..1440				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
ORIGIN					
Query Match	100.0%;	Score 601;	DB 6;	Length 1440;	
Best Local Similarity	100.0%;	Pred. No. 3.4e-160;			
Matches 601;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	CAGATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC	60		



Db 465 CAGATGTGGCTGACGTGAGTCTGAAAGGGTGGGATCATTGTTGAC 524  
Qy 61 TTCTGGACTATTATGAAAAATCAACACAGCAAGGAGTCCACACCCCTGCAGTCA 120  
Db 525 TTCTGGACTATTATGAAAAATCAACACAGCAAGGAGTCCACACCCCTGCAGTCA 584  
Qy 121 CTGGCTGTGAATGCAAGAAAGCAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180  
Db 585 CTGGCTGTGAATGCAAGAAAGCAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 644  
Qy 181 GGGCAGGACCACTTGAATTTCTGCCCTGCACACTGGAATTTGGAGAGCAGCAGAACCCAGG 240  
Db 645 GGGCAGGACCACTTGAATTTCTGCCCTGCACACTGGAATTTGGAGAGCAGCAGAACCCAGG 704  
Qy 241 GCCTGGCCCAACCAAGCTGGAGTGGAAAGGCAACAAGATTCCGGCCAGGCAGAAACAGGGCC 300  
Db 705 GCCTGGCCCAACCAAGCTGGAGTGGAAAGGCAACAAGATTCCGGCCAGGCAGAAACAGGGCC 764  
Qy 301 TACCTGGAGAGGACTGCTCCCTGCACAGCTGCAGCAGTTCGTGGAGCTGGGGAGAGGTGTT 360  
Db 765 TACCTGGAGAGGACTGCTCCCTGCACAGCTGCAGCAGTTCGTGGAGCTGGGGAGAGGTGTT 824  
Qy 361 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACC 420  
Db 825 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACC 884  
Qy 421 ACTCTACGGTGTGGGCTTTGAATCTACTACCCCAAGAAATCAACATGAAGTGGCTGAAG 480  
Db 885 ACTCTACGGTGTGGGCTTTGAATCTACTACCCCAAGAAATCAACATGAAGTGGCTGAAG 944  
Qy 481 GATAAGCAGCAATGGAATGCAAGGAGTTGCAACCTAAAGACGTATTGGCCCAATGGGGAT 540  
Db 945 GATAAGCAGCAATGGAATGCAAGGAGTTGCAACCTAAAGACGTATTGGCCCAATGGGGAT 1004  
Qy 541 GGGACCTACAGGGCTGGATAACCTTGGCTGTATACCCCTGGGGAAGCAGAGATATACG 600  
Db 1005 GGGACCTACAGGGCTGGATAACCTTGGCTGTATACCCCTGGGGAAGCAGAGATATACG 1064  
Qy 601 T 601  
Db 1065 T 1065

RESULT 7  
AR117795  
LOCUS 1440 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 11 from patent US 6140305.  
ACCESSION AR117795  
VERSION AR117795.1 GI:14098701  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1440)  
AUTHORS Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D., Tsuchihashi, Z. and Wolff, R.K.  
TITLE Hereditary hemochromatosis gene products  
JOURNAL Patent: US 6140305-A 11 31-OCT-2000;  
FEATURES Location/Qualifiers  
source 1..1440  
/organism="unknown"  
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ORIGIN  
Query Match 100.0%; Score 601; DB 6; Length 1440;  
Best Local Similarity 100.0%; Pred. No. 3.4e-160;  
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CAGATGTGGCTGACGTGAGTCTGAAAGGGTGGGATCACAATGTTCACTGTTGAC 60  
Db 465 CAGATGTGGCTGACGTGAGTCTGAAAGGGTGGGATCACAATGTTCACTGTTGAC 524  
Qy 61 TTCTGGACTATTATGAAAAATCAACACAGCAAGGAGTCCACACCCCTGCAGGTCA 120

Db 525 TTCTGGACTATTATGAAAAATCAACACAGCAAGGAGTCCACACCCCTGCAGTCA 584  
Qy 121 CTGGCTGTGAATGCAAGAAAGCAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180  
Db 585 CTGGCTGTGAATGCAAGAAAGCAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 644  
Qy 181 GGGCAGGACCACTTGAATTTCTGCCCTGCACACTGGAATTTGGAGAGCAGCAGAACCCAGG 240  
Db 645 GGGCAGGACCACTTGAATTTCTGCCCTGCACACTGGAATTTGGAGAGCAGCAGAACCCAGG 704  
Qy 241 GCCTGGCCCAACCAAGCTGGAGTGGAAAGGCAACAAGATTCCGGCCAGGCAGAAACAGGGCC 300  
Db 705 GCCTGGCCCAACCAAGCTGGAGTGGAAAGGCAACAAGATTCCGGCCAGGCAGAAACAGGGCC 764  
Qy 301 TACCTGGAGAGGACTGCTCCCTGCACAGCTGCAGCAGTTCGTGGAGCTGGGGAGAGGTGTT 360  
Db 765 TACCTGGAGAGGACTGCTCCCTGCACAGCTGCAGCAGTTCGTGGAGCTGGGGAGAGGTGTT 824  
Qy 361 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACC 420  
Db 825 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACC 884  
Qy 421 ACTCTACGGTGTGGGCTTTGAATCTACTACCCCAAGAAATCAACATGAAGTGGCTGAAG 480  
Db 885 ACTCTACGGTGTGGGCTTTGAATCTACTACCCCAAGAAATCAACATGAAGTGGCTGAAG 944  
Qy 481 GATAAGCAGCAATGGAATGCAAGGAGTTGCAACCTAAAGACGTATTGGCCCAATGGGGAT 540  
Db 945 GATAAGCAGCAATGGAATGCAAGGAGTTGCAACCTAAAGACGTATTGGCCCAATGGGGAT 1004  
Qy 541 GGGACCTACAGGGCTGGATAACCTTGGCTGTATACCCCTGGGGAAGCAGAGATATACG 600  
Db 1005 GGGACCTACAGGGCTGGATAACCTTGGCTGTATACCCCTGGGGAAGCAGAGATATACG 1064  
Qy 601 T 601  
Db 1065 T 1065

RESULT 8  
AR117796  
LOCUS 1440 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 12 from patent US 6140305.  
ACCESSION AR117796  
VERSION AR117796.1 GI:14098702  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1440)  
AUTHORS Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D., Tsuchihashi, Z. and Wolff, R.K.  
TITLE Hereditary hemochromatosis gene products  
JOURNAL Patent: US 6140305-A 12 31-OCT-2000;  
FEATURES Location/Qualifiers  
source 1..1440  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 601; DB 6; Length 1440;  
Best Local Similarity 100.0%; Pred. No. 3.4e-160;  
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CAGATGTGGCTGACGTGAGTCTGAAAGGGTGGGATCACAATGTTCACTGTTGAC 60  
Db 465 CAGATGTGGCTGACGTGAGTCTGAAAGGGTGGGATCACAATGTTCACTGTTGAC 524  
Qy 61 TTCTGGACTATTATGAAAAATCAACACAGCAAGGAGTCCACACCCCTGCAGGTCA 120  
Db 525 TTCTGGACTATTATGAAAAATCAACACAGCAAGGAGTCCACACCCCTGCAGGTCA 584







QY 181 GGGCAGGACCACTTGAATTTCTGCTTGAACACTGATTTGGAGAGCAGAGCAACCCAGG 240  
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Db 645 GGGCAGGACCACTTGAATTTCTGCTTGAACACTGATTTGGAGAGCAGAGCAACCCAGG 704  
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QY 241 GCCTGGCCCAACCAAGCTGGAGTGGGAAGGCAACAAGTTTGGGCCCAAGGCAACAGGGCC 300  
|||||  
Db 705 GCCTGGCCCAACCAAGCTGGAGTGGGAAGGCAACAAGTTTGGGCCCAAGGCAACAGGGCC 764  
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QY 301 TACTCTGGAGAGGAGCTGCCCTTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGCAGAGGTGTT 360  
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Db 765 TACTCTGGAGAGGAGCTGCCCTTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGCAGAGGTGTT 824  
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QY 361 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTTCAGTGAAC 420  
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Db 825 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTTCAGTGAAC 884  
|||||  
QY 421 ACTCTACGGTGTGGGCCCTTGAACCTACCTACCCCAAGACATCACCATGAAGTGGCTGAAG 480  
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QY 481 GATAAGCAGCAATGGATGCAAGGAGTTTGAACCTTAAAGACCTATTGGCCCAATGGGGAT 540  
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QY 541 GGGACCTACAGGGCTGGATAACCTTTGGCTGTATACCCCTGGGGAAGCAGAGATATACG 600  
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Db 1005 GGGACCTACAGGGCTGGATAACCTTTGGCTGTATACCCCTGGGGAAGCAGAGATATACG 1064  
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QY 601 T 601  
Db 1065 T 1065

RESULT 11  
AR149465  
LOCUS AR149465 1440 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 11 from patent US 6228594.  
ACCESSION AR149465  
VERSION AR149465.1 GI:151114056  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1440)  
AUTHORS Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,  
Tsuchihashi,Z. and Wolff,R.K.  
TITLE Method for determining the presence or absence of a hereditary  
hemochromatosis gene mutation  
JOURNAL Patent: US 6228594-A 11 08-MAY-2001;  
FEATURES Location/Qualifiers  
source 1. .1440  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 601; DB 6; Length 1440;  
Best Local Similarity 100.0%; Pred. No. 3.4e-160;  
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAGATGTGGCTGCAGCTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTGAC 60  
Db 465 CAGATGTGGCTGCAGCTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTGAC 524  
QY 61 TTCTGGACTATTATGAAATACACACAGCAGAGGAGTCCACACCTTCAGGTCATC 120  
Db 525 TTCTGGACTATTATGAAATACACACAGCAGAGGAGTCCACACCTTCAGGTCATC 584  
QY 121 CTGGGCTGTGAAATGCAAGAAGCAACAGTACCGAGGGCTACTTGGAAAGTACGGGTATGAT 180  
Db 585 CTGGGCTGTGAAATGCAAGAAGCAACAGTACCGAGGGCTACTTGGAAAGTACGGGTATGAT 644  
QY 181 GGGCAGGACCACTTGAATTTCTGCTTGAACACTGATTTGGAGAGCAGAGCAACCCAGG 240  
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Db 645 GGGCAGGACCACTTGAATTTCTGCTTGAACACTGATTTGGAGAGCAGAGCAACCCAGG 704  
QY 241 GCCTGGCCCAACCAAGCTGGAGTGGGAAGGCAACAAGTTTGGGCCCAAGGCAACAGGGCC 300  
Db 705 GCCTGGCCCAACCAAGCTGGAGTGGGAAGGCAACAAGTTTGGGCCCAAGGCAACAGGGCC 764  
QY 301 TACTCTGGAGAGGAGCTGCCCTTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGCAGAGGTGTT 360  
Db 765 TACTCTGGAGAGGAGCTGCCCTTGCACAGCTGCAGCAGTTGCTGGAGCTGGGGCAGAGGTGTT 824  
QY 361 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTTCAGTGAAC 420  
Db 825 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTTCAGTGAAC 884  
QY 421 ACTCTACGGTGTGGGCCCTTGAACCTACCTACCCCAAGACATCACCATGAAGTGGCTGAAG 480  
Db 885 ACTCTACGGTGTGGGCCCTTGAACCTACCTACCCCAAGACATCACCATGAAGTGGCTGAAG 944  
QY 481 GATAAGCAGCAATGGATGCAAGGAGTTTGAACCTTAAAGACCTATTGGCCCAATGGGGAT 540  
Db 945 GATAAGCAGCAATGGATGCAAGGAGTTTGAACCTTAAAGACCTATTGGCCCAATGGGGAT 1004  
QY 541 GGGACCTACAGGGCTGGATAACCTTTGGCTGTATACCCCTGGGGAAGCAGAGATATACG 600  
Db 1005 GGGACCTACAGGGCTGGATAACCTTTGGCTGTATACCCCTGGGGAAGCAGAGATATACG 1064  
QY 601 T 601  
Db 1065 T 1065

RESULT 12  
AR149466  
LOCUS AR149466 1440 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 12 from patent US 6228594.  
ACCESSION AR149466  
VERSION AR149466.1 GI:151114057  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1440)  
AUTHORS Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,  
Tsuchihashi,Z. and Wolff,R.K.  
TITLE Method for determining the presence or absence of a hereditary  
hemochromatosis gene mutation  
JOURNAL Patent: US 6228594-A 12 08-MAY-2001;  
FEATURES Location/Qualifiers  
source 1. .1440  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 601; DB 6; Length 1440;  
Best Local Similarity 100.0%; Pred. No. 3.4e-160;  
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAGATGTGGCTGCAGCTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTGAC 60  
Db 465 CAGATGTGGCTGCAGCTCAGAGTCTGAAAGGGTGGGATCACATGTTCACTGTGAC 524  
QY 61 TTCTGGACTATTATGAAATACACACAGCAGAGGAGTCCACACCTTCAGGTCATC 120  
Db 525 TTCTGGACTATTATGAAATACACACAGCAGAGGAGTCCACACCTTCAGGTCATC 584  
QY 121 CTGGGCTGTGAAATGCAAGAAGCAACAGTACCGAGGGCTACTTGGAAAGTACGGGTATGAT 180  
Db 585 CTGGGCTGTGAAATGCAAGAAGCAACAGTACCGAGGGCTACTTGGAAAGTACGGGTATGAT 644  
QY 181 GGGCAGGACCACTTGAATTTCTGCTTGAACACTGATTTGGAGAGCAGAGCAACCCAGG 240  
Db 645 GGGCAGGACCACTTGAATTTCTGCTTGAACACTGATTTGGAGAGCAGAGCAACCCAGG 704  
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QY 241 GCCTGGCCACCACCAAGCTGGAGTGGGAAGGCAACAGATTCCGGCCAGGCAGAACAGGGCC 300  
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QY 301 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTTCCTGGAGCTGGGGAGAGGTGTT 360  
DB 765 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTTCCTGGAGCTGGGGAGAGGTGTT 824  
QY 361 TTGGACCAACAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 420  
DB 825 TTGGACCAACAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 884  
QY 421 ACTCTACGGTGTGGGCCCTTGAACCTTACCCCAAGACATCACCATGAAGTGGCTGAAG 480  
DB 885 ACTCTACGGTGTGGGCCCTTGAACCTTACCCCAAGACATCACCATGAAGTGGCTGAAG 944  
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QY 541 GGGACCTACAGGGCTGGATTAACCTTGGCTGTACCCCTGGGGAGAGCAGAGATATACG 600  
DB 1005 GGGACCTACAGGGCTGGATTAACCTTGGCTGTACCCCTGGGGAGAGCAGAGATATACG 1064  
QY 601 T 601  
DB 1065 T 1065

RESULT 13  
AR199238  
LOCUS AR199238 2506 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 1 from patent US 6355425.  
ACCESSION AR199238  
VERSION AR199238.1 GI:20249312  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2506)  
AUTHORS Rothenberg,B.E., Sawada-Hirai,R. and Barton,J.C.  
TITLE Mutations associated with iron disorders  
JOURNAL Patent: US 6355425-A 1 12-MAR-2002;  
FEATURES Location/Qualifiers  
source  
1..2506  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 601; DB 6; Length 2506;  
Best Local Similarity 100.0%; Pred. No. 3.5e-160;  
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACAATGTTCACTGTTGAC 60  
DB 244 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACAATGTTCACTGTTGAC 303  
QY 61 TTCTGGACTATTATGAAAATCACAACCAAGAGGTGCCATGTTCACTGAGTCAATC 120  
DB 304 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACAATGTTCACTGTTGAC 303  
QY 121 TTCTGGACTATTATGAAAATCACAACCAAGAGGTGCCATGTTCACTGAGTCAATC 180  
DB 304 TTCTGGACTATTATGAAAATCACAACCAAGAGGTGCCATGTTCACTGAGTCAATC 363  
QY 121 CTGGGCTGTGAAATGCAAGAGACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180  
DB 364 CTGGGCTGTGAAATGCAAGAGACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 423  
QY 181 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAGG 240  
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QY 241 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAGG 300  
DB 484 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAGG 543  
QY 301 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTTCCTGGAGCTGGGGAGAGGTGTT 360  
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QY 301 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTTCCTGGAGCTGGGGAGAGGTGTT 360  
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QY 361 TTGGACCAACAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 420  
DB 604 TTGGACCAACAAGTGCCTCCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 663  
QY 421 ACTCTACGGTGTGGGCCCTTGAACCTTACCCCAAGACATCACCATGAAGTGGCTGAAG 480  
DB 664 ACTCTACGGTGTGGGCCCTTGAACCTTACCCCAAGACATCACCATGAAGTGGCTGAAG 723  
QY 481 GATAAGCAGCAATGATGCCAAGAGTTCGAACCTTAAAGACGTATTGCCCAATGGGGAT 540  
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QY 541 GGGACCTACAGGGCTGGATTAACCTTGGCTGTACCCCTGGGGAGAGCAGAGATATACG 600  
DB 784 GGGACCTACAGGGCTGGATTAACCTTGGCTGTACCCCTGGGGAGAGCAGAGATATACG 843  
QY 601 T 601  
DB 844 T 844

RESULT 14  
AR275757  
LOCUS AR275757 2506 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 1 from patent US 6509442.  
ACCESSION AR275757  
VERSION AR275757.1 GI:29709314  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2506)  
AUTHORS Rothenberg,B.E., Sawada-Hirai,R. and Barton,J.C.  
TITLE Mutations associated with iron disorders  
JOURNAL Patent: US 6509442-A 1 21-JAN-2003;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 100.0%; Score 601; DB 6; Length 2506;  
Best Local Similarity 100.0%; Pred. No. 3.5e-160;  
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACAATGTTCACTGTTGAC 60  
DB 244 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACAATGTTCACTGTTGAC 303  
QY 61 TTCTGGACTATTATGAAAATCACAACCAAGAGGTGCCATGTTCACTGAGTCAATC 120  
DB 304 TTCTGGACTATTATGAAAATCACAACCAAGAGGTGCCATGTTCACTGAGTCAATC 363  
QY 121 CTGGGCTGTGAAATGCAAGAGACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180  
DB 364 CTGGGCTGTGAAATGCAAGAGACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 423  
QY 181 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAGG 240  
DB 424 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAGG 483  
QY 241 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAGG 300  
DB 484 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAGG 543  
QY 301 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTTCCTGGAGCTGGGGAGAGGTGTT 360  
DB 544 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTTCCTGGAGCTGGGGAGAGGTGTT 603



Qy 361 TTGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACC 420  
Db 604 TTGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACC 663  
Qy 421 ACTCTACGGTGTGGGCTTGAACCTACTACTACCCAGAACATCACCATTGAAGTGGCTGAAG 480  
Db 664 ACTCTACGGTGTGGGCTTGAACCTACTACTACCCAGAACATCACCATTGAAGTGGCTGAAG 723  
Qy 481 GATAAGCAGCAATGGATGCCAAGAGTTCGAACCTTAAAGACGTATTGCCCAATGGGGAT 540  
Db 724 GATAAGCAGCAATGGATGCCAAGAGTTCGAACCTTAAAGACGTATTGCCCAATGGGGAT 783  
Qy 541 GGGACCTACCAAGGCTGATTAACCTTGGCTGTACCCCTGGGGAAGACAGAGATATACG 600  
Db 784 GGGACCTACCAAGGCTGATTAACCTTGGCTGTACCCCTGGGGAAGACAGAGATATACG 843  
Qy 601 T 601  
Db 844 T 844

RESULT 15

Q0717466  
LOCUS Q0717466 2716 bp DNA linear PAT 03-FEB-2004  
DEFINITION Sequence 3400 from Patent WO02068579.  
ACCESSION Q0717466  
VERSION Q0717466.1 GI:42278323  
KEYWORDS  
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1  
Venter, C.J., Adams M.C., Li, P.W. and Myers, E.W.  
Kits, such as nucleic acid arrays, comprising a majority of  
humanexons or transcripts, for detecting expression and other uses  
thereof

JOURNAL

Patent: WO 02068579-A 3400 06-SEP-2002;

PE Corporation (NY) (US)

FEATURES

source  
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Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 601; DB 6; Length 2716;  
Best Local Similarity 100.0%; Pred. No. 3.6e-160;  
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAGGGTGGGATCAGATGTTCACTGTTGAC 60  
Db 465 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAGGGTGGGATCAGATGTTCACTGTTGAC 524  
Qy 61 TTCTGGACTATTATGGAATAATCAACACAGCAAGAGTCCACACCCCTGCAGGTCATC 120  
Db 525 TTCTGGACTATTATGGAATAATCAACACAGCAAGAGTCCACACCCCTGCAGGTCATC 584  
Qy 121 CTGGGCTGTGAATGCAAGAGACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180  
Db 585 CTGGGCTGTGAATGCAAGAGACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 644  
Qy 181 GGGCAGGACCACCTTGAATTTCTCCCTGCACACTGGATTGGAGAGCAGCAACCCAGG 240  
Db 645 GGGCAGGACCACCTTGAATTTCTCCCTGCACACTGGATTGGAGAGCAGCAACCCAGG 704  
Qy 241 GCCTGGCCCAACAGCTGGAGTGGGAAGGCAACAAGATTCCGGCCAGGCAGAGAACAGGCC 300  
Db 705 GCCTGGCCCAACAGCTGGAGTGGGAAGGCAACAAGATTCCGGCCAGGCAGAGAACAGGCC 764  
Qy 301 TACTGAGAGGAGGACTGCCCTTCACAGCTGCAGAGTTGCTGGAGCTGGGAGAGGTGTT 360  
Db 765 TACTGAGAGGAGGACTGCCCTTCACAGCTGCAGAGTTGCTGGAGCTGGGAGAGGTGTT 824

Qy 361 TTGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACC 420  
Db 825 TTGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACC 884  
Qy 421 ACTCTACGGTGTGGGCTTGAACCTACTACTACCCAGAACATCACCATTGAAGTGGCTGAAG 480  
Db 885 ACTCTACGGTGTGGGCTTGAACCTACTACTACCCAGAACATCACCATTGAAGTGGCTGAAG 944  
Qy 481 GATAAGCAGCAATGGATGCCAAGAGTTCGAACCTTAAAGACGTATTGCCCAATGGGGAT 540  
Db 945 GATAAGCAGCAATGGATGCCAAGAGTTCGAACCTTAAAGACGTATTGCCCAATGGGGAT 1004  
Qy 541 GGGACCTACCAAGGCTGATTAACCTTGGCTGTACCCCTGGGGAAGACAGAGATATACG 600  
Db 1005 GGGACCTACCAAGGCTGATTAACCTTGGCTGTACCCCTGGGGAAGACAGAGATATACG 1064  
Qy 601 T 601  
Db 1065 T 1065

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Job time : 2570.56 secs



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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 05:14:23 ; Search time 307.314 Seconds  
(without alignments)

11576.980 Million cell updates/sec

Title: US-09-497-957-9\_COPY\_465\_1065

Perfect score: 601

Sequence: 1 CAGATGTGCTGCAGCTGAG.....GGAGAGCAGAGATATACCT 601

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2002bs:\*

8: Geneseqn2003as:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004as:\*

13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	601	100.0	1317	6	ABK49917 DNA encod
2	601	100.0	1439	10	ADG87336 Hereditar
3	601	100.0	1439	10	ADG87270 Hereditar
4	601	100.0	1439	10	ADG87268 Hereditar
5	601	100.0	1439	10	ADG87271 Hereditar
6	601	100.0	1439	10	ADG87269 Hereditar
7	601	100.0	1440	2	AAT96691 Hereditar
8	601	100.0	1440	5	AAC68430 Human her
9	601	100.0	1440	5	AAC68429 Human her
10	601	100.0	1440	5	AAC68431 Human her
11	601	100.0	1440	5	AAC68432 Human her
12	601	100.0	2506	3	AAG96769 cDNA sequ
13	601	100.0	2727	2	AAT23525 Haemochro
14	601	100.0	2727	11	ADP64956 Human hem
15	601	100.0	2727	11	ADP65373 Human hae
16	599	99.7	2285	13	ADQ38608 Human SNP
17	599	99.7	2426	13	ADQ38606 Human SNP
18	599	99.7	2716	13	ADQ38602 Human SNP
19	505	84.0	2674	13	ADQ38604 Human SNP
20	502.8	83.7	2231	13	ADQ38601 Human SNP

21	408.8	68.0	2189	13	ADQ38605	Adg38605 Human SNP
22	377	62.7	789	10	ADB50714	Adb50714 Primary r
23	377	62.7	1706	10	ADB57810	Adb57810 Toxicity-
24	277	46.1	282	12	ACH90634	Ach90634 Human gen
25	277	46.1	500	12	ACH76934	Ach76934 Human mus
26	277	46.1	5749	4	AAL36747	Aal36747 Human mus
27	277	46.1	5749	8	ABX59735	Abx59735 cDNA enco
28	277	46.1	5749	12	ADJ30485	Adj30485 Human mus
29	277	46.1	5982	8	ABV93934	Abv93934 Human col
30	277	46.1	10824	10	ADG87338	Adg87338 Hereditar
31	277	46.1	10824	10	ADG87266	Adg87266 Hereditar
32	277	46.1	10825	2	AAT96690	Aat96690 Hereditar
33	277	46.1	10825	5	AAC68426	Aac68426 Human her
34	277	46.1	10825	5	AAC68427	Aac68427 Human her
35	277	46.1	10825	5	AAC68428	Aac68428 Human her
36	277	46.1	10825	5	AAC68425	Aac68425 Human her
37	277	46.1	10825	10	ADG87260	Adg87260 Hereditar
38	277	46.1	10825	10	ADG87262	Adg87262 Hereditar
39	277	46.1	10825	10	ADG87264	Adg87264 Hereditar
40	277	46.1	12146	3	AAAG6794	Aaa96794 Genomic D
41	277	46.1	235033	2	AAV57926	Aav57926 Hereditar
42	277	46.1	237326	2	AAV57903	Aav57903 Hereditar
43	260.6	43.4	596	4	AAI63897	Aai63897 Human pol
44	260.6	43.4	596	12	ADM24448	Adm24448 Human PRO
45	232	38.6	359	2	AAAX16055	Aax16055 Hereditar

#### ALIGNMENTS

RESULT 1

ABK49917

ID ABK49917 standard; cDNA; 1317 BP.

XX AC ABK49917;

XX DT 15-JUL-2002 (first entry)

XX DE DNA encoding beta 2 microglobulin (beta2M)/HFE monochain.

XX KW Human; beta 2 microglobulin; beta2M/HFE monochain; HFE; ischaemia;

XX KW iron absorption regulator; intracellular iron absorption; lung injury;

XX KW haemochromatosis; transfusion; thalassaemia; haemolytic anaemia;

XX KW chronic infection; transferrin receptor; Tfr; brain tumour; cancer;

XX KW oxidative stress disorder; tissue damage; vascular disease; inflammation;

XX KW atherosclerosis; autoimmune disease; inflammatory condition; gene; ss.

XX OS Homo sapiens.

XX FH Key

XX CDS Location/Qualifiers

FT 1..1317

FT /\*tag= a

FT /product= "beta2M/HFE monochain"

FT WO200224929-A2.

XX PN 28-MAR-2002.

XX PD 24-SEP-2001; 2001WO-US029873.

XX PF 22-SEP-2000; 2000US-0234843P.

XX PR (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

XX PA (MCIN/) MCINNIS P.

XX PI Ehrlich R, Rotem-Yehudar R, Laham N;

XX DR WPI; 2002-383192/41.

XX DR P-PSDB; AAU80035.

XX PT Soluble beta 2 microglobulin/HFE monochain useful for treating iron-

XX PT overload conditions e.g. thalassaemia and chronic infections, comprises

XX PT human beta 2 microglobulin linked to alpha domains of HFE by a linker



PT peptide.  
XX  
PS Example 2; Fig 2; 77pp; English.  
XX  
CC The invention relates to a soluble polypeptide (I) of beta 2  
CC microglobulin (beta2m)/HFE monochain comprising human beta2m (or its  
CC analogue or active fragment), linked to alpha1-alpha3 domains of human  
CC HFE (a central regulator of iron absorption; undefined), or its analogue  
CC or active fragment, by a flexible linker peptide, or a functional  
CC derivative or salt of (I). (I) is useful for reducing intracellular iron  
CC absorption in patients having hereditary haemochromatosis, transfusions,  
CC thalassaemias, haemolytic anaemia or chronic infections, and for  
CC delivering a therapeutic to cells that over-express transferrin receptor  
CC (TfR) which are preferably lymphocytes or leukocytes, across the blood-  
CC brain barrier. (I) is further useful for treating brain tumour. (I) is  
CC also useful for treating oxidative stress disorders resulting in tissue  
CC damage e.g. vascular diseases, inflammation, atherosclerosis, lung  
CC injury, ischaemia, etc. A DNA molecule (II) encoding (I) is useful as a  
CC platform for drug delivery of therapeutic use for cancer, autoimmune  
CC diseases and inflammatory conditions. The monochain manifests specific  
CC characteristics advantageous for drug delivery systems. It is a soluble,  
CC stable and fully conformed protein. It binds specifically to transferrin  
CC receptor (TfR) and therefore targets cells that over-express this  
CC receptor. It is continuously internalised by the target cells, thus  
CC enabling efficient drug delivery. It dissociates from the receptor in the  
CC cells, minimising side effects. It negatively regulates iron absorption,  
CC reducing growth of undesired cells and preventing lymphocyte activation.  
CC It is not diluted in the blood as is transferrin. It should not induce an  
CC immune response since it is a self non-polymeric protein and delivery of  
CC drugs via monochain is expected to overcome drug-resistance since it is a  
CC natural TfR-binding protein. The present sequence represents the coding  
CC sequence of beta2m/HFE monochain  
XX  
SQ Sequence 1317 BP; 320 A; 325 C; 367 G; 305 T; 0 U; 0 Other;  
Query Match 100.0%; Score 601; DB 6; Length 1317;  
Best Local Similarity 100.0%; Pred. No. 5.4e-160;  
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAGATGTGGCTGCAGTGCAGTGTCTGAAAGGGTGGGATCATGTTCATCTTGAC 60  
DB 580 CAGATGTGGCTGCAGTGCAGTGTCTGAAAGGGTGGGATCATGTTCATCTTGAC 639  
QY 61 TTCTGGACTATTATGGAATAATCAACACAGCAGGAGTCCACACCTCGAGTGCATC 120  
DB 640 TTCTGGACTATTATGGAATAATCAACACAGCAGGAGTCCACACCTCGAGTGCATC 699  
QY 121 CTGGGCTGTGAAATCAAGAACACACAGTACCAGGGGCTACTGGAAGTACGGGTATGAT 180  
DB 700 CTGGGCTGTGAAATCAAGAACACACAGTACCAGGGGCTACTGGAAGTACGGGTATGAT 759  
QY 181 GGGCAGGACCACTTGAATTTGCGCTGCACACACTGGATTTGGAGAGCAGAACCCAGG 240  
DB 760 GGGCAGGACCACTTGAATTTGCGCTGCACACACTGGATTTGGAGAGCAGAACCCAGG 819  
QY 241 GCCTGGCCCAACAAGCTGGAGTGGGAAGGACACAGATTCGGCCGAGCAGCAACAGGCC 300  
DB 820 GCCTGGCCCAACAAGCTGGAGTGGGAAGGACACAGATTCGGCCGAGCAGCAACAGGCC 879  
QY 301 TACCTGGAGAGGAGTGCCTGCACAGTGTGCAGCAGTGTGCTGGAGCTGGGAGAGGTGT 360  
DB 880 TACCTGGAGAGGAGTGCCTGCACAGTGTGCAGCAGTGTGCTGGAGCTGGGAGAGGTGT 939  
QY 361 TTGGACCAACAAGTGCCTTGTGTGTGAGGTGACATCATGTGACCTTTCAGTGACC 420  
DB 940 TTGGACCAACAAGTGCCTTGTGTGTGAGGTGACATCATGTGACCTTTCAGTGACC 999  
QY 421 ACTCTACGGTGTGCGGCTTGAACCTACTACCCCGAAGACATCACCATGAGTGGCTGAAG 480  
DB 1000 ACTCTACGGTGTGCGGCTTGAACCTACTACCCCGAAGACATCACCATGAGTGGCTGAAG 1059  
QY 481 GATAAGCAGCCAAATGGATGCCAAGGAGTTTGCAGACCTTAAAGAGCTATTGCCCAATGGGAT 540  
|||||

DB 1060 GATAGCAGCCCAATGGATGGATGCCAAGAGTTGCAACCTAAGACGTATTGCCCAATGGGAT 1119  
QY 541 GGGACCTACAGGGCTGGATTAACCTTGTCTGTACCCCTGGGGAAAGACAGATATACG 600  
|||||  
DB 1120 GGGACCTACAGGGCTGGATTAACCTTGTCTGTACCCCTGGGGAAAGACAGATATACG 1179  
QY 601 T 601  
DB 1180 T 1180  
RESULT 2  
ADG87336  
ID ADG87336 standard; cDNA; 1439 BP.  
XX AC ADG87336;  
XX DT 11-MAR-2004 (first entry)  
XX DE Hereditary haemochromatosis (HH) 24d7 mutant cDNA.  
XX KW Hereditary haemochromatosis; HH; inherited disorder; iron metabolism;  
XX KW cirrhosis; diabetes; illness; gene therapy; hepatotropic; mutant; gene;  
XX KW ss.  
XX OS Unidentified.  
XX FH Key Location/Qualifiers  
XX CDS 222..1268  
XX FT /\*tag= a  
XX FT /product= "Hereditary haemochromatosis 24d7 mutant  
XX FT protein"  
XX PN US2003148972-A1.  
XX PD 07-AUG-2003.  
XX PF 02-MAY-2002; 2002US-00138888.  
XX PR 04-APR-1996; 96US-00630912.  
XX PR 16-APR-1996; 96US-00632673.  
XX PR 23-MAY-1996; 96US-00652265.  
XX PR 04-APR-1997; 97US-00834497.  
XX PR 04-FEB-2000; 2000US-00497957.  
XX PA (BIRA ) BIO-RAD LAB INC.  
XX PI Thomas WJ, Drayna DT, Feder JN, Gnirke A, Ruddy D, Tsuchihasi Z;  
XX Woff RK;  
XX DR WPI; 2003-897595/82.  
XX DR P-PSDB; ADG87337.  
XX PT New hereditary hemochromatosis (HH) nucleic acids and peptides, useful  
XX PT for treating HH leading to diabetes, cirrhosis, sterility or other  
XX PT serious illnesses.  
XX PS Disclosure; SEQ ID NO 77; 122pp; English.  
XX CC The present invention relates to gene and mutations thereto, that are  
XX CC responsible for the disease hereditary haemochromatosis (HH). Sequences  
XX CC of the invention are useful for treating hereditary haemochromatosis  
XX CC which is an inherited disorder or iron metabolism where the body  
XX CC accumulates excess iron. The excess in iron leads to cirrhosis, diabetes,  
XX CC and other serious illnesses. The invention is also useful in gene  
XX CC therapy. The present sequence is hereditary haemochromatosis 24d7 mutant  
XX CC cDNA.  
XX SQ Sequence 1439 BP; 345 A; 355 C; 407 G; 332 T; 0 U; 0 Other;  
Query Match 100.0%; Score 601; DB 10; Length 1439;  
Best Local Similarity 100.0%; Pred. No. 5.6e-160;  
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 CAGATGTGGCTGCAGCTGAGTCAAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 60  
DB 465 CAGATGTGGCTGCAGCTGAGTCAAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 524  
QY 61 TTCTGACTATTATGGAATAATCAACACAGCAAGAGAGTCCACACCTCTGCAGGTCATC 120  
DB 525 TTCTGACTATTATGGAATAATCAACACAGCAAGAGAGTCCACACCTCTGCAGGTCATC 584  
QY 121 CTGGGCTGTGAATGCAAGAGCAACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 180  
DB 585 CTGGGCTGTGAATGCAAGAGCAACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 644  
QY 181 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGAATTGGAGAGCAGCAAGCCAGG 240  
DB 645 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGAATTGGAGAGCAGCAAGCCAGG 704  
QY 241 GCCTGGCCCAACAGCTGGAGTGGGAAGGCAAGATTCGGGCCAGGCAAGAACAGGGCC 300  
DB 705 GCCTGGCCCAACAGCTGGAGTGGGAAGGCAAGATTCGGGCCAGGCAAGAACAGGGCC 764  
QY 301 TACTCTGAGAGGACTGCCCTGCACAGCTGCAGCAGTTCGTGGAGCTGGGGAGGTGTT 360  
DB 765 TACTCTGAGAGGACTGCCCTGCACAGCTGCAGCAGTTCGTGGAGCTGGGGAGGTGTT 824  
QY 361 TTGGACCAACAAGTGCCTCTCTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGAAC 420  
DB 825 TTGGACCAACAAGTGCCTCTCTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGAAC 884  
QY 421 ACTCTACGGTGTGGGGCTTGAACCTACTACCCCAAGATCCATCAAGTGGCTGAAG 480  
DB 885 ACTCTACGGTGTGGGGCTTGAACCTACTACCCCAAGATCCATCAAGTGGCTGAAG 944  
QY 481 GATAAGCAGCAATGATGCCAGGTTGCAACCTTAAGACGTATTGCCCAATGGGAT 540  
DB 945 GATAAGCAGCAATGATGCCAGGTTGCAACCTTAAGACGTATTGCCCAATGGGAT 1004  
QY 541 GGGACCTACAGGGCTGGATAACCTTTGGCTGTACCCCTGGGGAAGAGCAGATATACG 600  
DB 1065 T 1065

RESULT 3  
ADG87270  
ID ADG87270 standard; cdna; 1439 BP.  
XX AC  
XX ADG87270;  
XX DT 11-MAR-2004 (first entry)  
XX DE Hereditary haemochromatosis (HH) 24d2 mutant cdna.  
XX KW Hereditary haemochromatosis; HH; inherited disorder; iron metabolism;  
XX KW cirrhosis; diabetes; illness; gene therapy; hepatotropic; mutant; gene;  
XX KW 88.  
XX OS Unidentified.  
XX FH Key Location/Qualifiers  
XX CDS 222..1268  
XX FT /\*tag= a  
XX FT /product= "Hereditary haemochromatosis 24d2 mutant  
XX FT protein"  
XX US2003148972-A1.  
XX PN  
XX PD 07-AUG-2003.  
XX PF 02-MAY-2002; 2002US-00138888.

XX 04-APR-1996; 96US-00630912.  
PR 16-APR-1996; 96US-00632673.  
PR 23-MAY-1996; 96US-00652265.  
PR 04-APR-1997; 97US-00834497.  
PR 04-FEB-2000; 2000US-00497957.  
XX (BIRA ) BIO-RAD LAB INC.  
PA  
XX Thomas WJ, Drayna DT, Feder JN, Gnirke A, Ruddy D, Teuchihaashi Z;  
PI Wolff RK;  
XX WPI; 2003-897595/82.  
DR P-PSDB; ADG87265.  
XX New hereditary hemochromatosis (HH) nucleic acids and peptides, useful  
DR for treating HH leading to diabetes, cirrhosis, sterility or other  
XX serious illnesses.  
XX Claim 1; SEQ ID NO 11; 122pp; English.  
XX The present invention relates to gene and mutations thereto, that are  
CC responsible for the disease hereditary haemochromatosis (HH). Sequences  
CC of the invention are useful for treating hereditary haemochromatosis  
CC which is an inherited disorder or iron metabolism where the body  
CC accumulates excess iron. The excess in iron leads to cirrhosis, diabetes,  
CC and other serious illnesses. The invention is also useful in gene  
CC therapy. The present sequence is hereditary haemochromatosis 24d2 mutant  
CC cdna.  
XX  
SQ Sequence 1439 BP; 346 A; 354 C; 408 G; 331 T; 0 U; 0 Other;  
Query Match 100.0%; Score 601; DB 10; Length 1439;  
Best Local Similarity 100.0%; Pred. No. 5.6e-160;  
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAGATGTGGCTGCAGTCAAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 60  
DB 465 CAGATGTGGCTGCAGTCAAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 524  
QY 61 TTCTGACTATTATGGAATAATCAACACAGCAAGAGTCCACACCTCTGCAGGTCATC 120  
DB 525 TTCTGACTATTATGGAATAATCAACACAGCAAGAGTCCACACCTCTGCAGGTCATC 584  
QY 121 CTGGGCTGTGAATGCAAGAGCAACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 180  
DB 585 CTGGGCTGTGAATGCAAGAGCAACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 644  
QY 181 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAAGCCAGG 240  
DB 645 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAAGCCAGG 704  
QY 241 GCCTGGCCCAACAGCTGGAGTGGGAAGGCAAGATTCGGGCCAGGCAAGAACAGGGCC 300  
DB 705 GCCTGGCCCAACAGCTGGAGTGGGAAGGCAAGATTCGGGCCAGGCAAGAACAGGGCC 764  
QY 301 TACTCTGAGAGGACTGCCCTGCACAGCTGCAGCAGTTCGTGGAGCTGGGGAGGTGTT 360  
DB 765 TACTCTGAGAGGACTGCCCTGCACAGCTGCAGCAGTTCGTGGAGCTGGGGAGGTGTT 824  
QY 361 TTGGACCAACAAGTGCCTCTCTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGAAC 420  
DB 825 TTGGACCAACAAGTGCCTCTCTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGAAC 884  
QY 421 ACTCTACGGTGTGGGGCTTGAACCTACTACCCCAAGATCCATCAAGTGGCTGAAG 480  
DB 885 ACTCTACGGTGTGGGGCTTGAACCTACTACCCCAAGATCCATCAAGTGGCTGAAG 944  
QY 481 GATAAGCAGCAATGATGCCAGGTTGCAACCTTAAGACGTATTGCCCAATGGGAT 540  
DB 945 GATAAGCAGCAATGATGCCAGGTTGCAACCTTAAGACGTATTGCCCAATGGGAT 1004  
QY 541 GGGACCTACAGGGCTGGATAACCTTTGGCTGTACCCCTGGGGAAGAGCAGATATACG 600



Db 1005 GGGACCTACAGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGAGATATACG 1064  
601 T 601  
1065 T 1065

RESULT 4  
ADG87268  
ID ADG87268 standard; cDNA; 1439 BP.  
XX  
AC ADG87268;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Hereditary haemochromatosis (HH) wild-type cDNA.  
XX  
KW Hereditary haemochromatosis; HH; inherited disorder; iron metabolism;  
KW cirrhosis; diabetes; illness; gene therapy; hepatotropic; gene;  
KW chromosome 6; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT CDS 222..1268  
FT /\*tag= a  
FT /product= "Hereditary haemochromatosis wild-type protein"  
FT mutation replace(408.G)  
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FT /note= "24d2 mutation"  
FT mutation replace(414.T)  
FT /\*tag= c  
FT /note= "24d7 mutation"  
FT mutation replace(1066.A)  
FT /\*tag= d  
FT /note= "24d1 mutation"

US2003148972-A1.  
XX  
XX 07-AUG-2003.  
XX  
XX 02-MAY-2002; 2002US-00138888.  
XX  
XX 04-APR-1996; 96US-00630912.  
XX 16-APR-1996; 96US-00632673.  
XX 23-MAY-1996; 96US-00652265.  
XX 04-APR-1997; 97US-00834497.  
XX 04-FEB-2000; 2000US-00497957.  
XX  
XX (BIRA ) BIO-RAD LAB INC.  
XX  
XX Thomas WJ, Drayna DT, Feder JN, Gnirke A, Ruddy D, Tsuchihashi Z;  
XX Wolff RK;  
XX  
XX WPI; 2003-897595/82.  
XX P-PSDB; ADG87261.  
XX  
XX New hereditary hemochromatosis (HH) nucleic acids and peptides, useful  
XX for treating HH leading to diabetes, cirrhosis, sterility or other  
XX serious illnesses.  
XX  
XX Claim 1; SEQ ID NO 9; 122pp; English.  
XX  
XX The present invention relates to gene and mutations thereto, that are  
XX responsible for the disease hereditary haemochromatosis (HH). Sequences  
XX of the invention are useful for treating hereditary haemochromatosis  
XX which is an inherited disorder or iron metabolism where the body  
XX accumulates excess iron. The excess in iron leads to cirrhosis, diabetes,  
XX and other serious illnesses. The invention is also useful in gene  
XX therapy. The present sequence is hereditary haemochromatosis wild-type  
XX cDNA. HH gene is located on chromosome 6.

SQ Sequence 1439 BP; 346 A; 355 C; 407 G; 331 T; 0 U; 0 Other;  
Query Match 100.0%; Score 601; DB 10; Length 1439;  
Best Local Similarity 100.0%; Pred. No. 5.6e-160;  
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 465 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAGGGTGGGATCACATGTTCACTGTTGAC 524  
QY 61 TTCTGGACTATTATGAAAAATCACAACACAGCAGCAGGAGTCCACACACCTGCAGGTCAATC 120  
DB 525 TTCTGGACTATTATGAAAAATCACAACACAGCAGCAGGAGTCCACACACCTGCAGGTCAATC 584  
QY 121 CTGGGCTGTGAAATGCAAGAGACAAACAGTACCAGGGCTACTGGAAGTACGGGTATGAT 180  
DB 585 CTGGGCTGTGAAATGCAAGAGACAAACAGTACCAGGGCTACTGGAAGTACGGGTATGAT 644  
QY 181 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAGG 240  
DB 645 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAGG 704  
QY 241 GCCTGCCCAACCAAGCTGGAGTGGGAAAGGCACAAGATTTCGGGCCAGGCAGAACCCAGG 300  
DB 705 GCCTGCCCAACCAAGCTGGAGTGGGAAAGGCACAAGATTTCGGGCCAGGCAGAACCCAGG 764  
QY 301 TACCTGGAGAGGAGTGCCTGCACAGCTGCAGCAGTGTGGAGCTGGGGAGAGGTGTT 360  
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QY 481 GATAAGCAGCCAAATGGATGCCAAGAGTTCGAACCTAAAGAGTATTGCCCAATGGGGAT 540  
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QY 541 GGGACCTACAGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACG 600  
DB 1005 GGGACCTACAGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACG 1064  
QY 601 T 601  
DB 1065 T 1065

RESULT 5  
ADG87271  
ID ADG87271 standard; cDNA; 1439 BP.  
XX  
XX ADG87271;  
XX  
XX 11-MAR-2004 (first entry)  
XX  
XX Hereditary haemochromatosis (HH) mutant cDNA.  
XX  
XX Hereditary haemochromatosis; HH; inherited disorder; iron metabolism;  
XX cirrhosis; diabetes; illness; gene therapy; hepatotropic; mutant; gene;  
XX ss.  
XX  
XX Unidentified.  
XX  
XX Key Location/Qualifiers  
XX CDS 222..1268  
XX /\*tag= a  
XX /product= "Hereditary haemochromatosis mutant protein  
XX comprising 24d1 and 24d2 mutations."



PN US2003148972-A1.  
XX 07-AUG-2003.  
XX 02-MAY-2002; 2002US-00138888.  
XX 04-APR-1996; 96US-00630912.  
PR 16-APR-1996; 96US-00632673.  
PR 23-MAY-1996; 96US-00652265.  
PR 04-APR-1997; 97US-00834497.  
PR 04-FEB-2000; 2000US-00497957.  
XX (BIRA ) BIO-RAD LAB INC.  
XX Thomas WJ, Drayna DT, Feder JN, Gnirke A, Ruddy D, Tsuchihashi Z;  
PI Wolff RK;  
DR WPI; 2003-897595/82.  
DR P-PSDB; ADG87267.  
XX New hereditary hemochromatosis (HH) nucleic acids and peptides, useful  
PT for treating HH leading to diabetes, cirrhosis, sterility or other  
PT serious illnesses.  
XX Claim 1; SEQ ID NO 12; 122pp; English.  
XX The present invention relates to gene and mutations thereto, that are  
CC responsible for the disease hereditary haemochromatosis (HH). Sequences  
CC of the invention are useful for treating hereditary haemochromatosis  
CC which is an inherited disorder or iron metabolism where the body  
CC accumulates excess iron. The excess in iron leads to cirrhosis, diabetes,  
CC and other serious illnesses. The invention is also useful in gene  
CC therapy. The present sequence is hereditary haemochromatosis mutant CDNA  
CC comprising 24d1 and 24d2 mutations.  
XX Sequence 1439 BP; 347 A; 354 C; 407 G; 331 T; 0 U; 0 Other;  
SQ Query Match 100.0%; Score 601; DB 10; Length 1439;  
Best Local Similarity 100.0%; Pred. No. 5.6e-160;  
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAGATGTGGCTGAGCTGAGTCTGAAAGGTGGATCACATGTTCACTGTGAC 60  
Db 465 CAGATGTGGCTGAGCTGAGTCTGAAAGGTGGATCACATGTTCACTGTGAC 524  
QY 61 TTCTGACTATTATGAAATCAACACAGGAGTCCACACCCCTGCAGGTCATC 120  
Db 525 TTCTGACTATTATGAAATCAACACAGGAGTCCACACCCCTGCAGGTCATC 584  
QY 121 CTGGGCTGTGAATGCAAGAGACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180  
Db 585 CTGGGCTGTGAATGCAAGAGACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 544  
QY 181 GGCAGGACACCTTGAATTCCTGACACACTGGATTTGGAGACAGACAGCCAGG 240  
Db 645 GGCAGGACACCTTGAATTCCTGACACACTGGATTTGGAGACAGACAGCCAGG 704  
QY 241 GCTGGCCACCAAGCTGGAGTGGGAAGCACAAGATTGGGCCAGGACAGAGGCC 300  
Db 705 GCTGGCCACCAAGCTGGAGTGGGAAGCACAAGATTGGGCCAGGACAGAGGCC 764  
QY 301 TACCTGGAGGAGCTGCCTCTGACACAGCTGCAGCAGTGTCTGGAGCTGGGGAGAGGTGT 360  
Db 765 TACCTGGAGGAGCTGCCTCTGACACAGCTGCAGCAGTGTCTGGAGCTGGGGAGAGGTGT 824  
QY 361 TTGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCACTGACC 420  
Db 825 TTGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCACTGACC 884  
QY 421 ACTCTACGGTGTGGGCTTGAAGTACTACCTACCTACCTACCTACCTACCTACCTACCT 480  
Db 885 ACTCTACGGTGTGGGCTTGAAGTACTACCTACCTACCTACCTACCTACCTACCTACCT 944

QY 481 GATAAGCAGCAATGATGATGCAAGAGTTCGAACCTAAAGACCTATTGCCAATGGGAT 540  
Db 945 GATAAGCAGCAATGATGATGCAAGAGTTCGAACCTAAAGACCTATTGCCAATGGGAT 1004  
QY 541 GGGACCTACAGGGCTGGATTAACCTTGGCTGTACCCCTGGGGAAGACAGATATACG 600  
Db 1005 GGGACCTACAGGGCTGGATTAACCTTGGCTGTACCCCTGGGGAAGACAGATATACG 1064  
QY 601 T 601  
Db 1065 T 1065

RESULT 6  
ADG87269  
ID ADG87269 standard; CDNA; 1439 BP.  
XX AC ADG87269;  
XX 11-MAR-2004 (first entry)  
XX Hereditary haemochromatosis (HH) 24d1 mutant CDNA.  
XX Hereditary haemochromatosis; HH; inherited disorder; iron metabolism;  
KW cirrhosis; diabetes; illness; gene therapy; hepatotropic; mutant; gene;  
KW ss.  
XX Unidentified.  
XX Key Location/Qualifiers  
FT CDS 222..1268  
FT /tag= a  
FT /product= "Hereditary haemochromatosis 24d1 mutant  
FT protein"  
XX US2003148972-A1.  
XX 07-AUG-2003.  
XX 02-MAY-2002; 2002US-00138888.  
XX 04-APR-1996; 96US-00630912.  
PR 16-APR-1996; 96US-00632673.  
PR 23-MAY-1996; 96US-00652265.  
PR 04-APR-1997; 97US-00834497.  
PR 04-FEB-2000; 2000US-00497957.  
XX (BIRA ) BIO-RAD LAB INC.  
XX Thomas WJ, Drayna DT, Feder JN, Gnirke A, Ruddy D, Tsuchihashi Z;  
PI Wolff RK;  
DR WPI; 2003-897595/82.  
DR P-PSDB; ADG87263.  
XX New hereditary hemochromatosis (HH) nucleic acids and peptides, useful  
PT for treating HH leading to diabetes, cirrhosis, sterility or other  
PT serious illnesses.  
XX Claim 1; SEQ ID NO 10; 122pp; English.  
XX The present invention relates to gene and mutations thereto, that are  
CC responsible for the disease hereditary haemochromatosis (HH). Sequences  
CC of the invention are useful for treating hereditary haemochromatosis  
CC which is an inherited disorder or iron metabolism where the body  
CC accumulates excess iron. The excess in iron leads to cirrhosis, diabetes,  
CC and other serious illnesses. The invention is also useful in gene  
CC therapy. The present sequence is hereditary haemochromatosis 24d1 mutant  
CC CDNA.  
XX Sequence 1439 BP; 347 A; 355 C; 406 G; 331 T; 0 U; 0 Other;  
SQ Query Match 100.0%; Score 601; DB 10; Length 1439;



Best Local Similarity 100.0%; Pred. No. 5.6e-160;		Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTTCATCTGTGAC	60
Db	465	CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTTCATCTGTGAC	524
QY	61	TTCTGGACTATTATGGAATAACAAACACAGAGAGAGTCCACACCCCTGCAGGTCTATC	120
Db	525	TTCTGGACTATTATGGAATAACAAACACAGAGAGAGTCCACACCCCTGCAGGTCTATC	584
QY	121	CTGGGCTGTGAATGCAGAGACACAGTACCGAGGGCTACTGGAAGTACCGGTATGAT	180
Db	585	CTGGGCTGTGAATGCAGAGACACAGTACCGAGGGCTACTGGAAGTACCGGTATGAT	644
QY	181	GGCGAGGACACCTTGAATTCCTCCCTGCACACACTGGATTGGAGAGCAGACAGACCCAGG	240
Db	645	GGCGAGGACACCTTGAATTCCTCCCTGCACACACTGGATTGGAGAGCAGACAGACCCAGG	704
QY	241	GCCTGGCCCAACAGTGGAGTGGGAAGGCAACAGATTTCGGGCCAGGCAACAGGGCC	300
Db	705	GCCTGGCCCAACAGTGGAGTGGGAAGGCAACAGATTTCGGGCCAGGCAACAGGGCC	764
QY	301	TACCTGGAGAGGACTGCCTCTGCACAGCTGCAGAGTTGCTGAGCTGGGGAGAGTGT	360
Db	765	TACCTGGAGAGGACTGCCTCTGCACAGCTGCAGAGTTGCTGAGCTGGGGAGAGTGT	824
QY	361	TTGGACCAACAAGTGCTCTTTTGGTGAAGTGACACATCATGTGACCTTTTCAGTGACC	420
Db	825	TTGGACCAACAAGTGCTCTTTTGGTGAAGTGACACATCATGTGACCTTTTCAGTGACC	884
QY	421	ACTTACGTTGTGGGCTTTGAATCTACTACCCCGAAGACATCACATGAGTGGCTGAAG	480
Db	885	ACTTACGTTGTGGGCTTTGAATCTACTACCCCGAAGACATCACATGAGTGGCTGAAG	944
QY	481	GATAAGCAGCAATGATGCCAAGAGTTTCGAACCTTAAGACGTATTGCCCAATGGGAT	540
Db	945	GATAAGCAGCAATGATGCCAAGAGTTTCGAACCTTAAGACGTATTGCCCAATGGGAT	1004
QY	541	GGGACCTACAGGGCTGGATAACCTTTGGCTGTATACCCCTGGGGAAGAGCAGATATAG	600
Db	1005	GGGACCTACAGGGCTGGATAACCTTTGGCTGTATACCCCTGGGGAAGAGCAGATATAG	1064
QY	601	T 601	
Db	1065	T 1065	
RESULT 7			
AAT96691 standard; cDNA; 1440 BP.			
XX	AC	AAT96691;	
DT	14-APR-1998	(first entry)	
XX	Hereditary haemochromatosis gene cDNA clone.		
KW	Hereditary haemochromatosis; metal toxicity; diagnosis; gene therapy;		
KW	prenatal screening; human; ss.		
OS	Homo sapiens.		
PH	Key	Location/Qualifiers	
FT	CDS	222..1268	
FT	mutation	/*tag= a	
FT		408	
FT		/*tag= g	
FT		/note= "C to G substitution (24d2 mutation) results in	
FT	variation	His to Asp substitution"	
FT		414	
FT		/*tag= h	
FT		/note= "A to T substitution (24d7 variant) results in Ser	

FT	mutation	to Cys substitution"	
FT	1066		
FT	/*tag= i		
FT	/note= "G to A substitution (24d1 mutation associated		
FT	with HH), results in Cys to Tyr substitution"		
XX	WO9738137-A1.		
PD	16-OCT-1997.		
XX	04-APR-1997;	97WO-US006254.	
XX	04-APR-1996;	96US-00630912.	
PR	16-APR-1996;	96US-00632673.	
PR	23-MAY-1996;	96US-00652265.	
XX	(MERC-) MERCATOR GENETICS INC.		
XX	Thomas WJ, Drayna DT, Feder JN, Gnirke A, Ruddy D, Tsuchihashi Z;		
PI	Wolff RK;		
XX	WPI; 1997-512743/47.		
DR	P-PSDB; AAW36499.		
XX	Hereditary haemochromatosis gene and variants - useful for diagnosis and		
PT	treatment of hereditary haemochromatosis disease.		
XX	Disclosure; Fig 4; 115pp; English.		
PS	This cDNA clone, designated cDNA24, is derived from human gene whose		
CC	mutated form is associated with hereditary haemochromatosis (HH). It was		
CC	obtained from a directionally cloned plasmid-based cDNA library following		
CC	identification of the HH locus in the HLA region of chromosome 6. A		
CC	single mutation (24d1) in the HH gene appears responsible for the		
CC	majority of HH disease. This comprises a G to A substitution that is		
CC	present in 86% of affected chromosomes and in 4% of unaffected		
CC	chromosomes. It results in a Cys to Tyr substitution in the encoded		
CC	protein (see AAW36499) at a critical disulphide bridge important for		
CC	secondary structure. The following are claimed: a 10825 bp genomic DNA		
CC	sequence (I) (see AAT96690), the 1437 bp cDNA sequence (Ia) and their		
CC	24d1, 24d2 and 24d7 variants; a cloning or expression vector; host cells;		
CC	a peptide product chosen from the HH gene product, its variants (24d1,		
CC	24d2 and 24d7), or a peptide of at least 56 amino acid residues of these;		
CC	an antibody produced using the peptide; a method to determine the		
CC	presence or absence of the common HH gene mutation; an animal model for		
CC	the HH disease; metal chelation agents, T-cell differentiation factors		
CC	and therapeutic agents for the mitigation of injury due to oxidative		
CC	process in vivo or mitigation of iron overload; a method for screening		
CC	potential therapeutic agents for activity in connection with HH disease;		
CC	an antisense oligonucleotide directed against a transcriptional product		
CC	of a nucleic acid sequence as above; and oligonucleotides or pairs of		
CC	oligonucleotides covering a range of nucleotides from (I), (Ia) or their		
CC	variants, useful for detecting a polymorphism in the HH gene. The		
CC	invention also relates to methods for screening for HH homozygotes, to HH		
CC	diagnosis, prenatal screening and diagnosis, and therapies of HH disease,		
CC	including gene therapy, protein- and antibody-based therapeutics, and		
CC	small molecule therapeutics		
XX			
SQ	Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 U; 0 Other;		
Query Match 100.0%; Score 601; DB 2; Length 1440;			
Best Local Similarity 100.0%; Pred. No. 5.6e-160;			
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTTCATCTGTGAC	60
Db	465	CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCACATGTTTCATCTGTGAC	524
QY	61	TTCTGGACTATTATGGAATAACAAACACAGAGAGAGTCCACACCCCTGCAGGTCTATC	120
Db	525	TTCTGGACTATTATGGAATAACAAACACAGAGAGAGTCCACACCCCTGCAGGTCTATC	584
QY	121	CTGGGCTGTGAATGCAAGAGACACAGTACCGAGGGCTACTGGAAGTACCGGTATGAT	180



585 CTGGCTGTGAAATGCAAGAAGCAACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 644  
181 GGCAGAGCACCTTGAATTCGCCCTGACACACTGGATTGGAGAGCAGAACCCAGG 240  
645 GGGCAGAGCACCTTGAATTCGCCCTGACACACTGGATTGGAGAGCAGAACCCAGG 704  
241 GCCTGGCCCAACCAAGCTGGAGTGGAAAGGCAACAAGATTCCGGCCAGGCAGAACAGGGCC 300  
705 GCCTGGCCCAACCAAGCTGGAGTGGAAAGGCAACAAGATTCCGGCCAGGCAGAACAGGGCC 764  
301 TACTTGAGAGGAGCTGCCCTTGACACAGCTGCAGCAGTGTCTGGAGCTGGGGAGAGGTGT 360  
765 TACTTGAGAGGAGCTGCCCTTGACACAGCTGCAGCAGTGTCTGGAGCTGGGGAGAGGTGT 824  
361 TTGGACCAACAAGTGCCTCTTGGTGAAGTGACACATCATGTGACCTTTCAGTGACC 420  
825 TTGGACCAACAAGTGCCTCTTGGTGAAGTGACACATCATGTGACCTTTCAGTGACC 884  
421 ACTCTACGGTGTGGGCTTGAATCTACTACCCCAAGCAACATCAACCATGAAGTGGCTGAAG 480  
885 ACTCTACGGTGTGGGCTTGAATCTACTACCCCAAGCAACATCAACCATGAAGTGGCTGAAG 944  
481 GATAAGCAGCAATGATGCAAGAGTTCGAACCTAAAGACGTATTGGCCCAATGGGGAT 540  
945 GATAAGCAGCAATGATGCAAGAGTTCGAACCTAAAGACGTATTGGCCCAATGGGGAT 1004  
541 GGGACCTACAGGCTGGGATAAATCTGGCTGTACCCCTGGGGAAGCAGAGATATACG 600  
1005 GGGACCTACAGGCTGGGATAAATCTGGCTGTACCCCTGGGGAAGCAGAGATATACG 1064  
601 T 601  
1065 T 1065

RESULT 8  
AAC68430  
ID AAC68430 standard; DNA; 1440 BP.  
XX AC AAC68430;  
XX DT 21-FEB-2001 (first entry)  
XX Human hereditary hemochromatosis 24d1 mutation cDNA.  
XX HH; hereditary hemochromatosis; chelation agent;  
XX T-cell differentiation factor; iron overload; ss.  
XX Homo sapiens.  
XX US6140305-A.  
XX PD 31-OCT-2000.  
XX PF 04-APR-1997; 97US-00834497.  
XX PR 04-APR-1996; 96US-00630912.  
XX PR 16-APR-1996; 96US-00632673.  
XX PR 23-MAY-1996; 96US-00652265.  
XX PA (BIRA ) BIO-RAD LAB INC.  
XX PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;  
PI Feder JN;  
XX WPI; 2001-006341/01.  
XX New hereditary hemochromatosis gene products or polypeptides, useful for  
PT treating hereditary hemochromatosis in a patient, and as a metal  
PT chelation agent alleviating iron overload.  
XX PS Disclosure; Fig 4; 108pp; English.

XX The present invention relates to hereditary hemochromatosis gene  
CC products. These proteins may be used to treat a patient diagnosed as  
CC having human hemochromatosis disease. It is also useful as a metal  
CC chelation agent or as a T-cell differentiation factor, and for  
CC alleviating iron overload. They may also be used in protein replacement  
CC therapy for individuals having a defective human hemochromatosis gene  
XX Sequence 1440 BP; 348 A; 355 C; 406 G; 331 T; 0 U; 0 Other;  
Query Match 100.0%; Score 601; DB 5; Length 1440;  
Best Local Similarity 100.0%; Pred. No. 5.6e-160;  
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAGATCTGGCTGAGTGCAGTCTGAAAGGCTGGGATCAGATCTTCACTGTGAC 60  
DB 465 CAGATCTGGCTGAGTGCAGTCTGAAAGGCTGGGATCAGATCTTCACTGTGAC 524  
QY 61 TTCTGGACTATTATGAAATCAACACAGCAAGAGTCCACACCCCTGCAGGTCATC 120  
DB 525 TTCTGGACTATTATGAAATCAACACAGCAAGAGTCCACACCCCTGCAGGTCATC 584  
QY 121 CTGGGCTGTGAATCAAGAAGCAACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 180  
DB 585 CTGGGCTGTGAATCAAGAAGCAACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 644  
QY 181 GGGCAGGACCACTTGAATCTGCCCTGACACACTGGATTGGAGAGCAGAACCCAGG 240  
DB 645 GGGCAGGACCACTTGAATCTGCCCTGACACACTGGATTGGAGAGCAGAACCCAGG 704  
QY 241 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAACAAGATTCCGGCCAGGCAGAACAGGGCC 300  
DB 705 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAACAAGATTCCGGCCAGGCAGAACAGGGCC 764  
QY 301 TACTTGAGAGGAGCTGCCCTTGACACAGCTGCAGCAGTGTCTGGAGCTGGGGAGAGGTGT 360  
DB 765 TACTTGAGAGGAGCTGCCCTTGACACAGCTGCAGCAGTGTCTGGAGCTGGGGAGAGGTGT 824  
QY 361 TTGGACCAACAAGTGCCTCTTGGTGAAGTGACACATCATGTGACCTTTCAGTGACC 420  
DB 825 TTGGACCAACAAGTGCCTCTTGGTGAAGTGACACATCATGTGACCTTTCAGTGACC 884  
QY 421 ACTCTACGGTGTGGGCTTGAATCTACTACCCCAAGCAACATCAACCATGAAGTGGCTGAAG 480  
DB 885 ACTCTACGGTGTGGGCTTGAATCTACTACCCCAAGCAACATCAACCATGAAGTGGCTGAAG 944  
QY 481 GATAAGCAGCAATGATGCAAGAGTTCGAACCTAAAGACGTATTGGCCCAATGGGGAT 540  
DB 945 GATAAGCAGCAATGATGCAAGAGTTCGAACCTAAAGACGTATTGGCCCAATGGGGAT 1004  
QY 541 GGGACCTACAGGCTGGGATAAATCTGGCTGTACCCCTGGGGAAGCAGAGATATACG 600  
DB 1005 GGGACCTACAGGCTGGGATAAATCTGGCTGTACCCCTGGGGAAGCAGAGATATACG 1064  
QY 601 T 601  
DB 1065 T 1065

RESULT 9  
AAC68429  
ID AAC68429 standard; DNA; 1440 BP.  
XX AC AAC68429;  
XX DT 21-FEB-2001 (first entry)  
XX Human hereditary hemochromatosis cDNA.  
XX HH; hereditary hemochromatosis; chelation agent;  
XX T-cell differentiation factor; iron overload; ss.  
XX Homo sapiens.



XX US6140305-A.  
PN 31-OCT-2000.  
XX 04-APR-1997; 97US-00834497.  
XX 04-APR-1996; 96US-00630912.  
PR 16-APR-1996; 96US-00632673.  
PR 23-MAY-1996; 96US-00652265.  
XX (BIRA ) BIO-RAD LAB INC.  
XX Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;  
PI Feder JN;  
XX WPI; 2001-006341/01.  
XX New hereditary hemochromatosis gene products or polypeptides, useful for  
PT treating hereditary hemochromatosis in a patient, and as a metal  
PT chelation agent alleviating iron overload.  
XX Disclosure; Fig 4; 108pp; English.  
XX The present invention relates to hereditary hemochromatosis gene  
CC products. These proteins may be used to treat a patient diagnosed as  
CC having human hemochromatosis disease. It is also useful as a metal  
CC chelation agent or as a T-cell differentiation factor, and for  
CC alleviating iron overload. They may also be used in protein replacement  
CC therapy for individuals having a defective human hemochromatosis gene  
XX Sequence 1440 BP; 347 A; 355 C; 407 G; 331 T; 0 U; 0 Other;  
SQ Query Match 100.0%; Score 601; DB 5; Length 1440;  
Best Local Similarity 100.0%; Pred. No. 5.6e-160;  
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAGATGTGGCTGACGTGAGTCTGAAAGGGTGGGATCAGATGTTCACTGTGAC 60  
Db 465 CAGATGTGGCTGACGTGAGTCTGAAAGGGTGGGATCAGATGTTCACTGTGAC 524  
QY 61 TTCTGGACTATTATGAAATCACAACACAGCAGAGGAGTCCACACCTCGAGGTCATC 120  
Db 525 TTCTGGACTATTATGAAATCACAACACAGCAGAGGAGTCCACACCTCGAGGTCATC 584  
QY 121 CTGGGCTGTGAATGCAAGAGACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180  
Db 585 CTGGGCTGTGAATGCAAGAGACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 644  
QY 181 GGGCAGGACACCTTGAATTCGCCCTGACACACTGGATTGGAGAGCAGAGCCAGG 240  
Db 645 GGGCAGGACACCTTGAATTCGCCCTGACACACTGGATTGGAGAGCAGAGCCAGG 704  
QY 241 GCTGSCCCACCAAGCTGGAGTGGGAAAGGCAAGATTCCGGCCAGGAGAGGCGC 300  
Db 705 GCTGSCCCACCAAGCTGGAGTGGGAAAGGCAAGATTCCGGCCAGGAGAGGCGC 764  
QY 301 TACCTGGAGAGGAGTCCCTGCACAGCTGCAGCAGTTCCTCGAGCTGGGGAGAGTGT 360  
Db 765 TACCTGGAGAGGAGTCCCTGCACAGCTGCAGCAGTTCCTCGAGCTGGGGAGAGTGT 824  
QY 361 TTGGACCAACAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACC 420  
Db 825 TTGGACCAACAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGACC 884  
QY 421 ACTCTACGCTGTGGGCTTTGAATCTACTACCCCAAGACATCACCATTGAAGTGGCTGAAG 480  
Db 885 ACTCTACGCTGTGGGCTTTGAATCTACTACCCCAAGACATCACCATTGAAGTGGCTGAAG 944  
QY 481 GATAAGCAGCCAAATGGATGCCAAGGAGTTTCAACCTTAAAGACGTATTGCCCCAATGGGAT 540  
Db 945 GATAAGCAGCCAAATGGATGCCAAGGAGTTTCAACCTTAAAGACGTATTGCCCCAATGGGAT 1004

QY 541 GGGACCTACCGGCTGGATACCTTGGCTGTACCCCTGGGAAAGAGCAGAGATATACG 600  
Db 1005 GGGACCTACCGGCTGGATACCTTGGCTGTACCCCTGGGAAAGAGCAGAGATATACG 1064  
QY 601 T 601  
Db 1065 T 1065  
RESULT 10  
AAC68431  
ID AAC68431 standard; DNA; 1440 BP.  
XX AAC68431;  
AC AAC68431;  
XX 21-FEB-2001 (first entry)  
XX Human hereditary hemochromatosis 24d2 mutation cDNA.  
XX HH; hereditary hemochromatosis; chelation agent;  
KW T-cell differentiation factor; iron overload; ss.  
XX Homo sapiens.  
XX OS  
XX US6140305-A.  
XX 31-OCT-2000.  
XX 04-APR-1997; 97US-00834497.  
PR 04-APR-1996; 96US-00630912.  
PR 16-APR-1996; 96US-00632673.  
PR 23-MAY-1996; 96US-00652265.  
XX (BIRA ) BIO-RAD LAB INC.  
XX Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;  
PI Feder JN;  
XX WPI; 2001-006341/01.  
XX New hereditary hemochromatosis gene products or polypeptides, useful for  
PT treating hereditary hemochromatosis in a patient, and as a metal  
PT chelation agent alleviating iron overload.  
XX Disclosure; Fig 4; 108pp; English.  
XX The present invention relates to hereditary hemochromatosis gene  
CC products. These proteins may be used to treat a patient diagnosed as  
CC having human hemochromatosis disease. It is also useful as a metal  
CC chelation agent or as a T-cell differentiation factor, and for  
CC alleviating iron overload. They may also be used in protein replacement  
CC therapy for individuals having a defective human hemochromatosis gene  
XX Sequence 1440 BP; 347 A; 354 C; 408 G; 331 T; 0 U; 0 Other;  
SQ Query Match 100.0%; Score 601; DB 5; Length 1440;  
Best Local Similarity 100.0%; Pred. No. 5.6e-160;  
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAGATGTGGCTGACGTGAGTCTGAAAGGGTGGGATCAGATGTTCACTGTGAC 60  
Db 465 CAGATGTGGCTGACGTGAGTCTGAAAGGGTGGGATCAGATGTTCACTGTGAC 524  
QY 61 TTCTGGACTATTATGAAATCACAACACAGCAGAGGAGTCCACACCTCGAGGTCATC 120  
Db 525 TTCTGGACTATTATGAAATCACAACACAGCAGAGGAGTCCACACCTCGAGGTCATC 584  
QY 121 CTGGGCTGTGAATGCAAGAGACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180  
Db 585 CTGGGCTGTGAATGCAAGAGACACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 644  
QY 181 GGGCAGGACACCTTGAATTCGCCCTGACACACTGGATTGGAGAGCAGAGCCAGG 240



Db 645 GGCAGGACACCTTGAATTCGCTCCCTGACACACTGGATTTGGAGCAGCAGAACCCAGG 704  
 QY 241 GCCTGGCCCAACCAAGCTGGAGTGGAAAGGCAACAAGATTTCGGGCCAGGCAGAACAGGGCC 300  
 Db 705 GCCTGGCCCAACCAAGCTGGAGTGGAAAGGCAACAAGATTTCGGGCCAGGCAGAACAGGGCC 764  
 QY 301 TACCTGGAGAGGAGCTGCCCTGACACAGCTGCAGAGTGTCTGGAGCTGGGGAGAGGTGTT 360  
 Db 765 TACCTGGAGAGGAGCTGCCCTGACACAGCTGCAGAGTGTCTGGAGCTGGGGAGAGGTGTT 824  
 QY 361 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCACTGAC 420  
 Db 825 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCACTGAC 884  
 QY 421 ACTCTACGGTGTGGGGCTTTGAATCTACTACCCCGAGAACATCACCATTGAAGTGGCTGAAG 480  
 Db 885 ACTCTACGGTGTGGGGCTTTGAATCTACTACCCCGAGAACATCACCATTGAAGTGGCTGAAG 944  
 QY 481 GATAAGCAGCAATGGATGCCAAGGAGTTTCGAACCTTAAGACGTTATTTGCCCAATGGGGAT 540  
 Db 945 GATAAGCAGCAATGGATGCCAAGGAGTTTCGAACCTTAAGACGTTATTTGCCCAATGGGGAT 1004  
 QY 541 GGGACCTACAGGGCTGGATAACCTTGGCTGTATACCCCTGGGGAAGCAGAGATATACG 600  
 Db 1005 GGGACCTACAGGGCTGGATAACCTTGGCTGTATACCCCTGGGGAAGCAGAGATATACG 1064  
 QY 601 T 601  
 Db 1065 T 1065

RESULT 11  
 AAC68432  
 ID AAC68432 standard; DNA; 1440 BP.  
 AC AAC68432;  
 XX  
 XX 21-FEB-2001 (first entry)  
 XX Human hereditary hemochromatosis 24d1/2 mutation cDNA.  
 XX HH; hereditary hemochromatosis; chelation agent;  
 KW T-cell differentiation factor; iron overload; ss.  
 XX  
 XX Homo sapiens.  
 XX US6140305-A.  
 XX 31-OCT-2000.  
 XX 04-APR-1997; 97US-00834497.  
 XX 04-APR-1996; 96US-00630912.  
 XX 16-APR-1996; 96US-00632673.  
 XX 23-MAY-1996; 96US-00652265.  
 XX (BIRA ) BIO-RAD LAB INC.  
 XX Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;  
 PI Feder UN;  
 XX WPI; 2001-006341/01.  
 XX New hereditary hemochromatosis gene products or polypeptides, useful for  
 PT treating hereditary hemochromatosis in a patient, and as a metal  
 PT chelation agent alleviating iron overload.  
 XX  
 XX Disclosure; Fig 4; 108pp; English.  
 XX  
 XX The present invention relates to hereditary hemochromatosis gene  
 CC products. These proteins may be used to treat a patient diagnosed as  
 CC having human hemochromatosis disease. It is also useful as a metal

CC chelation agent or as a T-cell differentiation factor, and for  
 CC alleviating iron overload. They may also be used in protein replacement  
 CC therapy for individuals having a defective human hemochromatosis gene  
 XX  
 SQ Sequence 1440 BP; 348 A; 354 C; 407 G; 331 T; 0 U; 0 Other;  
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 Best Local Similarity 100.0%; Pred. No. 5.6e-160;  
 Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CAGATGTGCTGAGCTGAGTCTGAAAGGGTGGGATCAGATCAGATGTTCACTGTTGAC 60  
 Db 465 CAGATGTGCTGAGCTGAGTCTGAAAGGGTGGGATCAGATGTTCACTGTTGAC 524  
 QY 61 TTCTGACCTATTATGAAATCAACACAGCAGCAAGAGTCCACACCCCTGCAAGTTCATC 120  
 Db 525 TTCTGACCTATTATGAAATCAACACAGCAGCAAGAGTCCACACCCCTGCAAGTTCATC 584  
 QY 121 CTGGGCTGTGAAATGCAAGAAGCAACAGTACCGAGGCTACTTGGAAAGTACGGGTATGAT 180  
 Db 585 CTGGGCTGTGAAATGCAAGAAGCAACAGTACCGAGGCTACTTGGAAAGTACGGGTATGAT 644  
 QY 181 GGGCAGGACCACTTGAATTTGCTCCCTGACACACTGGATTGGAGAGCAGAACCCAGG 240  
 Db 645 GGGCAGGACCACTTGAATTTGCTCCCTGACACACTGGATTGGAGAGCAGAACCCAGG 704  
 QY 241 GCTGSCCCACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAAGACAGGCC 300  
 Db 705 GCTGSCCCACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAAGACAGGCC 764  
 QY 301 TACCTGGAGAGGAGCTGCCCTGACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTGTT 360  
 Db 765 TACCTGGAGAGGAGCTGCCCTGACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTGTT 824  
 QY 361 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCACTGAC 420  
 Db 825 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCACTGAC 884  
 QY 421 ACTCTACGGTGTGGGGCTTTGAATCTACTACCCCGAGAACATCACCATTGAAGTGGCTGAAG 480  
 Db 885 ACTCTACGGTGTGGGGCTTTGAATCTACTACCCCGAGAACATCACCATTGAAGTGGCTGAAG 944  
 QY 481 GATAAGCAGCAATGGATGCCAAGGAGTTTCGAACCTTAAGACGTTATTTGCCCAATGGGGAT 540  
 Db 945 GATAAGCAGCAATGGATGCCAAGGAGTTTCGAACCTTAAGACGTTATTTGCCCAATGGGGAT 1004  
 QY 541 GGGACCTACAGGGCTGGATAACCTTGGCTGTATACCCCTGGGGAAGCAGAGATATACG 600  
 Db 1005 GGGACCTACAGGGCTGGATAACCTTGGCTGTATACCCCTGGGGAAGCAGAGATATACG 1064  
 QY 601 T 601  
 Db 1065 T 1065  
 RESULT 12  
 AAA96769  
 ID AAA96769 standard; cDNA; 2506 BP.  
 XX  
 XX AAA96769;  
 AC  
 XX 19-FEB-2001 (first entry)  
 XX  
 XX cDNA sequence encoding a histocompatibility iron loading (HFE) protein.  
 XX Human; histocompatibility iron loading protein; HFE protein;  
 KW major histocompatibility complex; non-classical class I gene;  
 KW chromosome 6p; iron disorder; haemochromatosis; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH 1. .1044  
 FT CDS











Db 525 TTCTGGACTATTATGAAATACAAACCAAGAGGTCCACACCTTCAGGTATC 584  
Qy 121 CTGGGCTGTGAATCAAGAGACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180  
Db 585 CTGGGCTGTGAATCAAGAGACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 644  
Qy 181 GGGCAGGACCACTTGAATTCGCTGACACACTGGATTGGAGAGCAGACAACCCAGG 240  
Db 645 GGGCAGGACCACTTGAATTCGCTGACACACTGGATTGGAGAGCAGACAACCCAGG 704  
Qy 241 GCTGSCCCACCAAGCTGGAGTGGGAAAGGCAAGATTGCGGSCAGGCAGACAACAGGGCC 300  
Db 705 GCTGSCCCACCAAGCTGGAGTGGGAAAGGCAAGATTGCGGSCAGGCAGACAACAGGGCC 764  
Qy 301 TACCTGGAGAGGACTGCGCTTCGACAGCTGCAGCAGTTCGCTGGAGCTGGGGAGAGTGT 360  
Db 765 TACCTGGAGAGGACTGCGCTTCGACAGCTGCAGCAGTTCGCTGGAGCTGGGGAGAGTGT 824  
Qy 361 TTGGACCAACAGTGGCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 420  
Db 825 TTGGACCAACAGTGGCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 884  
Qy 421 ACTCTACGCTGTCGSCCTTGAATCTACTACCCCAAGACATCACCATGAAGTGGCTGAAG 480  
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Db 945 GATAAGCAGCCAAATGGATGCCAAGAGATTGCAACCTTAAAGACGTATTGCCCAATGGGAT 1004  
Qy 541 GGGACCTACAGGGCTGGATTAACCTTGGCTGTATACCCCTGGGGAAGAGAGATATACG 600  
Db 1005 GGGACCTACAGGGCTGGATTAACCTTGGCTGTATACCCCTGGGGAAGAGAGATATACG 1064  
Qy 601 T 601  
Db 1065 T 1065  
RESULT 15  
ID ADP65373  
AC ADP65373 standard; DNA; 2727 BP.  
XX ADP65373;  
DT 12-AUG-2004 (first entry)  
XX Human haemochromatosis protein (HLA-H) mRNA, complete cds DNA.  
XX autoimmune disease; arthritis; gene expression analysis;  
KW rheumatoid arthritis; collagen-induced; immunosuppressive; anti-rheumatic;  
KW antirheumatic; osteopathic; antigout; anti-inflammatory; dermatological;  
KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;  
KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;  
KW immune; ds; human.  
XX Homo sapiens.  
XX WO2003072827-A1.  
XX 04-SEP-2003.  
XX 31-OCT-2002; 2002WO-US035433.  
XX 31-OCT-2001; 2001US-0336220P.  
XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
XX Hirsch R, Thorton SL;  
PI WPI: 2003-712740/67.  
DR GENBANK, U60319.

XX Diagnosing and analyzing autoimmune disease using gene expression  
PT profiles and microarray technology, useful for diagnosing and treating  
PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and  
PT gout.  
XX Disclosure; Page; 56pp; English.  
XX The invention relates to a novel method for diagnosing and analysing  
CC autoimmune disease or arthritides. The method comprises obtaining a  
CC patient sample containing mRNA, analysing gene expression using the mRNA  
CC that results in a gene expression signature of the mRNA, and using that  
CC gene expression signature to diagnose or analyse the autoimmune disease  
CC or arthritides in the patient, where gene expression of at least 60% of  
CC the genes correlates with that of the gene signature. The invention  
CC further comprises: a treatment of rheumatoid arthritis; identification of  
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal;  
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an  
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or  
CC analyses of autoimmune disease or rheumatoid arthritis; screening the  
CC efficacy of a candidate drug in vitro for the treatment of collagen-  
CC induced arthritis; and reducing the symptoms associated with collagen-  
CC induced arthritis. The compositions of the invention have the following  
CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,  
CC antigout, anti-inflammatory, dermatological, and immunomodulatory. The  
CC methods and compositions of the present invention are useful for  
CC diagnosing and treating autoimmune disease or arthritides, such as  
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,  
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an  
CC immune disease caused by an infectious agent. This polynucleotide  
CC represents a DNA sequence relating to the genes used in the analysis and  
CC treatment of autoimmune diseases or arthritides. Note: This sequence is  
CC not shown in the specification. It has been supplied in an electronic  
CC format from WIPO.  
XX SQ Sequence 2727 BP; 702 A; 606 C; 660 G; 759 T; 0 U; 0 Other;  
Query Match 100.0%; Score 601; DB 11; Length 2727;  
Best Local Similarity 100.0%; Pred. No. 7.1e-160;  
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCATCATGTTTCATCTTGAC 60  
Db 465 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCATCATGTTTCATCTTGAC 524  
Qy 61 TTCTGGACTATTATGGAATAATCAACCAAGCAAGAGAGTCCCAACCCCTGCAGGTATC 120  
Db 525 TTCTGGACTATTATGGAATAATCAACCAAGCAAGAGAGTCCCAACCCCTGCAGGTATC 584  
Qy 121 CTGGGCTGTGAATGCAAGAGACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180  
Db 585 CTGGGCTGTGAATGCAAGAGACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 644  
Qy 181 GGGCAGGACCACTTGAATTCGCTGACACACTGGATTGGAGAGCAGACAACCCAGG 240  
Db 645 GGGCAGGACCACTTGAATTCGCTGACACACTGGATTGGAGAGCAGACAACCCAGG 704  
Qy 241 GCTTGGCCCAACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAGACAACAGGGCC 300  
Db 705 GCTTGGCCCAACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAGACAACAGGGCC 764  
Qy 301 TACCTGGAGAGGAGTGGCTTCGACAGCTGCAGCAGTTCGCTGGAGAGAGTGT 360  
Db 765 TACCTGGAGAGGAGTGGCTTCGACAGCTGCAGCAGTTCGCTGGAGAGAGTGT 824  
Qy 361 TTGGACCAACAGTGGCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 420  
Db 825 TTGGACCAACAGTGGCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 884  
Qy 421 ACTCTACGCTGTCGSCCTTGAATCTACTACCCCAAGACATCACCATGAAGTGGCTGAAG 480  
Db 885 ACTCTACGCTGTCGSCCTTGAATCTACTACCCCAAGACATCACCATGAAGTGGCTGAAG 944



Qy	481	GATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGAT	540
Db	945	GATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGAT	1004
Qy	541	GGGACCTACCAGGGCTGGTAACCTTGGCTGTACCCCTGGGGAAGACAGAGATATACG	600
Db	1005	GGGACCTACCAGGGCTGGTAACCTTGGCTGTACCCCTGGGGAAGACAGAGATATACG	1064
Qy	601	T	601
Db	1065	T	1065

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 Job time : 309.314 secs



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 09:06:57 ; Search time 1892.7 Seconds  
(without alignments)  
12086.738 Million cell updates/sec

Title: US-09-497-957-9\_COPY\_465\_1065  
Perfect score: 601  
Sequence: 1 CAGATGTGCTGCAGCTGAG.....GGAAGACGAGATATACCT 601

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsa1:\*  
9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	565	94.0	819	4	BG747345
2	491.8	81.8	570	2	BE272926
3	387	64.4	729	6	CB529554
4	359	59.7	1719	3	AK088986
5	359	59.7	1723	3	AK009581
6	350	58.2	603	7	CN264281
7	324.2	53.9	820	5	BP434195
8	282	46.9	560	1	AU279987
9	261.8	43.6	535	6	CB162561
10	260	43.3	544	4	BM751283
11	257.2	42.8	825	5	BU746849
12	251.4	41.8	457	1	AI850020
13	248.4	41.3	455	2	BE995172
14	244.6	40.7	542	6	CA569584
15	230	38.3	384	2	BF833952
16	229	38.1	871	5	BU746860
17	219	36.4	799	7	CK366555
18	214.6	35.7	546	2	BQ809138
19	199.6	33.2	481	5	BQ561639
20	178	29.6	668	4	BM723847
21	174	29.0	394	2	BF464345
22	160.4	26.7	645	1	AU296357
23	151.8	25.3	289	7	H33644
24	149.6	24.9	668	6	BY745026

ALIGNMENTS

RESULT 1	25	146	24.3	531	8	AQ703007	AQ703007 HS 5443 B
LOCUS	26	138.4	23.0	444	8	AZ025590	AZ025590 RPCI-23-3
DEFINITION	27	136.6	22.7	492	9	CG578705	CG578705 OST216218
ACCESSION	28	131.6	21.9	489	2	BE994943	BE994943 UI-M-CG0P
VERSION	29	130	21.6	807	7	COS71571	COS71571 AGENCOURT
KEYWORDS	30	129.6	21.6	737	5	BM919242	BM919242 AGENCOURT
SOURCE	31	129.6	21.6	1041	5	BM919242	BM919242 AGENCOURT
ORGANISM	32	129.4	21.5	579	5	BP333106	BP333106 BP333106
	33	129.2	21.5	550	4	BI339179	BI339179 364041 MA
	34	128.8	21.4	1005	6	BY705256	BY705256 BY705256
	35	128.8	21.4	1021	5	BM920008	BM920008 AGENCOURT
	36	128.8	21.4	1298	3	AK005051	AK005051 Mus muscu
	37	127.2	21.2	656	7	CK429585	CK429585 OJ38e12.Y
	38	127	21.1	979	7	COS79967	COS79967 ILLUMIGEN
	39	125.6	20.9	526	2	BF192528	BF192528 243759 MA
	40	125.6	20.9	582	1	AV691580	AV691580 AV691580
	41	124.8	20.8	521	2	BE808803	BE808803 214082 MA
	42	124.8	20.8	536	8	AZ074871	AZ074871 RPCI-23-4
	43	124.6	20.7	464	1	AA217236	AA217236 mu89b05.1
	44	124.6	20.7	763	7	COS68645	COS68645 AGENCOURT
	45	124.6	20.7	953	7	COS83074	COS83074 ILLUMIGEN

819 bp mRNA linear EST 15-MAY-2001  
602704818F1 NIH\_MGC\_15 Homo sapiens CDNA clone IMAGE:4857941 5',  
mRNA sequence.  
BG747345  
BG747345.1 GI:14057998  
EST.  
Homo sapiens (human)  
Homo sapiens  
Homo sapiens  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLM711 row: d column: 06  
High quality sequence stop: 792.  
Location/Qualifiers  
1. 819  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4857941"  
/tissue\_type="adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 15"  
/note="Organ: colon; Vector: pOTB7; Site: 1; XhoI; Site\_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"

Query Match 94.0%; Score 565; DB 4; Length 819;







## REFERENCE

1 (bases 1 to 729)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 Tissue Procurement: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-rc@mail.nih.gov](mailto:cgapbs-rc@mail.nih.gov)  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/cgap.html>  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

## FEATURES

## source

1..729  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-H-FT2-bjh-m-12-0-UI"  
 /tissue\_type="Alveolar Macrophage"  
 /dev\_stage="Adult"  
 /lab\_host="DR10B (Life Technologies)"  
 /clone\_lib="NCI\_CGAP\_FT2"  
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI CGAP FT2 is a subcloned cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subcloned according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG\_TISSUE=Human Lung Alveolar Macrophage

TAG\_LIB=UI-H-FT2

TAG\_SEQ=GGCCATGCGG

## ORIGIN

Query Match 64.4%; Score 387; DB 6; Length 729;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-95;  
 Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 275 AGATTCCGGCCAGGACAGACAGGGCTTACTCTGAGAGGAGTCTGCTCTGACAGCTGCAGC 334  
 DB 669 AGATTCCGGCCAGGACAGACAGGGCTTACTCTGAGAGGAGTCTGCTCTGACAGCTGCAGC 610  
 QY 335 AGTTGCTGGAGCTGGGGAGAGGTGTTTGGACCAACCAAGTCCCTCTTTGGTGAAGGTGA 394  
 DB 609 AGTTGCTGGAGCTGGGGAGAGGTGTTTGGACCAACCAAGTCCCTCTTTGGTGAAGGTGA 550  
 QY 395 CACATCATGTGACCTCTTTCAGTGACCACTCTACGGTGTGGGGCTTGAACCTACTACCCCC 454  
 DB 549 CACATCATGTGACCTCTTTCAGTGACCACTCTACGGTGTGGGGCTTGAACCTACTACCCCC 490

QY 455 AGAACATCATCATGAAGTGGCTCAAGGATAAGCAGCAATGGATGGCAAGGAGTTTGAAC 514  
 DB 489 AGAACATCATCATGAAGTGGCTCAAGGATAAGCAGCAATGGATGGCAAGGAGTTTGAAC 430  
 QY 515 CTAAGACAGCTATTGGCCCAATGGGGATGGGACCTTACAGGGCTGGATAACCTTGGCTGTAC 574  
 DB 429 CTAAGACAGCTATTGGCCCAATGGGGATGGGACCTTACAGGGCTGGATAACCTTGGCTGTAC 370  
 QY 575 CCCTGGGAGAGCAGCAGATATACCT 601  
 DB 369 CCCTGGGAGAGCAGCAGATATACCT 343

## RESULT 4

## AK088986

## LOCUS

## DEFINITION

## AK088986

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

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## AUTHORS

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## AUTHORS

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## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

AK088986 1719 bp mRNA linear HTC 03-APR-2004  
 Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN  
 full-length enriched library, clone:E430034J19  
 product:hemochromatosis, full insert sequence.

AK088986 1 GI:26354115  
 HTC; CAP trapper.  
 Mus musculus (house mouse)  
 Mus musculus  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)  
 99279253  
 10349636

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
 20493374  
 11042159

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kishimoto, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujisawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 20530913  
 11076861

4 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409, 685-690 (2001)

5 The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 6 (bases 1 to 1719)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,



Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.  
Direct Submission  
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

TITLE  
JOURNAL

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC Building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
Location/Qualifiers  
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QY 97 GAGTCCCAACCCCTGCAGGTCTATCTGGGCTGTGAAATGCAAGAACACAGTACCCGAG 156  
DB 469 GAGTCCCAACATCTGCAGGTGGTCTCTAGGCTGTGAGGTGCATGACGACCAACAGTACCAGC 528

QY 157 GGCTACTGGAAGTACGGCTGATGATGGGAGGACACCTTGAAATCTGCCTGACACACTG 216  
DB 529 GGCTTCTTGAGATATGGTTATGACGGGCAAGATACCTTGGAAATCTGCCCCAAGACACTA 588  
QY 217 GATTGGAGAGCAGCAGAAACCCAGGCGCTGGCCCAACCAAGCTGGAGTGGGAAAGGCACAAG 276  
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DEFINITION  
Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310032M04 product:hemochromatosis, full insert sequence.  
AK009581  
VERSION  
HTC; CAP trapper.  
KEYWORDS  
Mus musculus (house mouse)  
SOURCE  
Mus musculus  
ORGANISM  
Carninci, P. and Hayashizaki, Y.  
REFERENCE  
1  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
99279253  
10349636  
REFERENCE  
2  
AUTHORS  
TITLE  
JOURNAL  
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2049374  
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AUTHORS  
TITLE  
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MEDLINE  
PUBMED  
20530913  
11076861  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kusunagi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)



4 REFERENCE  
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
5 REFERENCE  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
6 REFERENCE  
AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furukuni, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Macsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscl.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
COMMENT Please visit our web site (<http://genome.gsc.riken.jp/>) for further details.  
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5', GAGAGAGAGAGATCAAGAGCTTTTCTTTTCTTTTCTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATCTCGATTAATTAATTAATCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.  
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QY 1 CAGATCTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 60  
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REFERENCE 1 (bases 1 to 603)  
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebowitz, J. and Stanton, L.W.  
TITLE Transcription characterization elucidates signaling networks that control human ES cell growth and differentiation  
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)  
COMMENT Contact: Brandenberger R



## Regenerative Medicine

Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
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## FEATURES

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## ORIGIN

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## RESULT 7

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LOCUS BP434195 full-length enriched swine cDNA library, adult lung Sus  
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VERSION BP434195.1  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa

## REFERENCE

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
TITLE Unishii, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H.,  
Okumura, N., Hamasima, N., and Awata, T.  
JOURNAL PEDE (Pig Est Data Explorer): construction of a database for ESTs  
COMMENT derived from porcine full-length cDNA libraries  
Nucleic Acids Res. 32 (1), D484-D488 (2004)  
Contact: Hirohide Unishii  
Animal Genome Laboratory, Genome Research Department  
National Institute of Agrobiological Sciences  
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan  
Tel: +81-29-838-8627

Fax: +81-29-838-8627

Email: huenishi@affrc.go.jp  
EST project with full-length enriched cDNA libraries carried out in  
Animal Genome Research Program (Japan) by National Institute of  
Agrobiological Sciences and STAFF-Institute  
Single pass sequencing of clones derived from oligo-capped cDNA  
library

Vector sequences were eliminated by RepeatMasker version 2002/07/13  
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Low quality bases were trimmed based on the quality values.

## FEATURES

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## ORIGIN

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## RESULT 8

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DEFINITION AU279987 sequence.  
ACCESSION AU279987  
VERSION AU279987.1 GI:28299214  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens



**REFERENCE**  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 560)  
 Imabayashi, H., Mori, T., Gojo, S., Kiyono, T., Sugiyama, T., Irie, R., Isogai, T., Hata, J., Tomoya, Y., and Umezawa, A.  
 Redifferentiation of dedifferentiated chondrocytes and chondrogenesis of human bone marrow stromal cells via chondrosphere formation with expression profiling by large-scale cDNA analysis  
 Exp. Cell Res. 288 (1), 35-50 (2003)  
 22760698  
 12878157  
 Contact: Takao Isogai  
 Genomics Laboratory  
 Helix Research Institute  
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 Tel: 81-438-52-3975  
 Fax: 81-438-52-3986  
 Email: genomics@hri.co.jp  
 HRI human cDNA Project, Sugiyama, T.; Wakamatsu, A.; Irie, R.; Umezawa, A.; Fukuma, M.; Kusakari, S.; Hata, J.; Ishii, S.; Yamamoto, J.; Isono, Y.; Saito, K.; Nakamura, Y.; Masuho, Y.; Nagai, K.; Isogai, T.  
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**ORIGIN**  
 Query Match 46.9%; Score 282; DB 1; Length 560;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-66;  
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGATGTGGCTGAGCTGAGTCTGAAAGGGTGGGATCACATGTTCTGCTGTGAC 60  
 Db 279 CAGATGTGGCTGAGCTGAGTCTGAAAGGGTGGGATCACATGTTCTGCTGTGAC 338  
 QY 61 TTCTGGACTATTATGGAATATCAACACAGCAAGGAGTCCACACCCCTGCAAGTATC 120  
 Db 339 TTCTGGACTATTATGGAATATCAACACAGCAAGGAGTCCACACCCCTGCAAGTATC 398  
 QY 121 CTGGGCTGTAATGCAAGAACACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 180  
 Db 399 CTGGGCTGTAATGCAAGAACACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 458  
 QY 181 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGAACCCAGG 240  
 Db 459 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGAACCCAGG 518  
 QY 241 GCCTGGCCCAACCAAGCTGAGTGGGAAAGGCACAAAGATTGG 282  
 Db 519 GCCTGGCCCAACCAAGCTGAGTGGGAAAGGCACAAAGATTGG 560

**RESULT** 9  
 CB162561  
 LOCUS  
 DEFINITION  
 K-EST0223175 L17N670205n1 Homo sapiens cDNA clone EST 30-JAN-2003  
 L17N670205n1-27-D07 5', mRNA sequence.  
 CB162561  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 535)  
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,

Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.  
 21C Frontier Korean EST Project 2001  
 Unpublished (2002)  
 Contact: Kim YS  
 Genomic Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongsung@mail.kribb.re.kr  
 Plate: 27 row: D column: 07  
 High quality sequence stop: 535.

**FEATURES**  
 source  
 1..535  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="L17N670205n1-27-D07"  
 /sex="F"  
 /lab\_host="Top10P"  
 /clone\_lib="L17N670205n1"  
 /note="Organ: Liver; Vector: pT7T3-Pac; Site 1: EcoRI; Site 2: NotI; The library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell culture."

**ORIGIN**  
 Query Match 43.6%; Score 261.8; DB 6; Length 535;  
 Best Local Similarity 99.2%; Pred. No. 1.1e-60;  
 Matches 263; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAGATGTGGCTGAGCTGAGTCTGAAAGGGTGGGATCACATGTTCTGCTGTGAC 60  
 Db 271 CAGATGTGGCTGAGCTGAGTCTGAAAGGGTGGGATCACATGTTCTGCTGTGAC 330  
 QY 61 TTCTGGACTATTATGGAATATCAACACAGCAAGGAGTCCACACCCCTGCAAGTATC 120  
 Db 331 TTCTGGACTATTATGGAATATCAACACAGCAAGGAGTCCACACCCCTGCAAGTATC 390  
 QY 121 CTGGGCTGTAATGCAAGAACACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 180  
 Db 391 CTGGGCTGTAATGCAAGAACACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 450  
 QY 181 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGAACCCAGG 240  
 Db 451 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGAACCCAGG 510  
 QY 241 GCCTGGCCCAACCAAGCTGAGTGGG 265  
 Db 511 GCCTGGCCCAACCAAGCTGAGTGGG 535

**RESULT** 10  
 BM751283  
 LOCUS  
 DEFINITION  
 K-EST0027329 S9SNU601 Homo sapiens cDNA clone S9SNU601-12-G03 5', mRNA sequence.  
 BM751283  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 544)  
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.  
 21C Frontier Korean EST Project 2001  
 Unpublished (2002)



## COMMENT

Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 12 row: G column: 03  
High quality sequence stop: 544.

## FEATURES

Location/Qualifiers  
1..544  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="S9SNU601-12-G03"  
/sex="M"  
/tissue\_type="Aescites"  
/cell\_type="Epithelial"  
/cell\_line="SNU-601"  
/lab\_host="Top10F"  
/clone\_lib="S9SNU601"  
/note="Organ: Stomach; Vector: pME18-FL3; Site: 1: XhoI; Site 2: XhoI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII- digested pME18-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F, by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

## Source

1..825  
/organism="Canis familiaris"  
/mol\_type="mRNA"  
/db\_xref="taxon:9615"  
/clone="CH3#007\_D04"  
/tissue\_type="heart"  
/cell\_type="heart"  
/dev\_stage="mixed developmental stages (adult, 30 day - 40 day fetal)"  
/clone\_lib="Canine heart normalized cDNA Library in pBluescript"  
/note="Organ: heart; Vector: pBluescript; Site: 1: 5' of vector NotI; Site 2: 3' of vector EcoRI; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction: oligo-dT primed"

## FEATURES

Location/Qualifiers

1..825

/organism="Canis familiaris"

/mol\_type="mRNA"

/db\_xref="taxon:9615"

/clone="CH3#007\_D04"

/tissue\_type="heart"

/cell\_type="heart"

/dev\_stage="mixed developmental stages (adult, 30 day - 40 day fetal)"

/clone\_lib="Canine heart normalized cDNA Library in pBluescript"

/note="Organ: heart; Vector: pBluescript; Site: 1: 5' of vector NotI; Site 2: 3' of vector EcoRI; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction: oligo-dT primed"

## ORIGIN

Query Match 43.3%; Score 260; DB 4; Length 544;  
Best Local Similarity 100.0%; Pred. No. 3.5e-60;  
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGTGGGATCACATGTTCACTGTTGAC 60  
|||  
Db 285 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGTGGGATCACATGTTCACTGTTGAC 344  
|||  
QY 61 TTCTGGACTATTATGAAATCACACACAGCAGGAGTCCACACCCCTGCAGGTCATC 120  
|||  
Db 345 TTCTGGACTATTATGAAATCACACACAGCAGGAGTCCACACCCCTGCAGGTCATC 404  
|||  
QY 121 CTGGGCTGTGAATGCAAGAACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180  
|||  
Db 405 CTGGGCTGTGAATGCAAGAACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 464  
|||  
QY 181 GGGCAGGACACCTTGAATTCGCCCTGACACACTGGATTGGAGCAGCAGAACCCAGG 240  
|||  
Db 465 GGGCAGGACACCTTGAATTCGCCCTGACACACTGGATTGGAGCAGCAGAACCCAGG 524  
|||  
QY 241 GCCTGGCCCCACCAAGCTGGA 260  
|||  
Db 525 GCCTGGCCCCACCAAGCTGGA 544  
|||

## RESULT 11

BU746849 825 bp mRNA linear EST 10-OCT-2002  
LOCUS CH3#007\_D04T7 Canine heart normalized cDNA Library in pBluescript  
DEFINITION Canis familiaris cDNA clone CH3#007\_D04 5', mRNA sequence.  
ACCESSION BU746849  
VERSION BU746849.1 GI:23697227  
KEYWORDS EST.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris

## REFERENCE

1. (bases 1 to 825)  
AUTHORS Yi, Y., Desai, R., Olarte, M., Henthorn, P. and George A. L.  
TITLE Expressed sequence tags from Canine heart  
JOURNAL Unpublished (2003)  
COMMENT Contact: George A. L.  
Division of Genetic Medicine  
Vanderbilt University  
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA  
Tel: 615 936 2660  
Fax: 615 936 2661  
Email: al.george@vanderbilt.edu  
Insert Length: 1739 Std Error: 0.00  
Seq primer: 17: TAATACGACTCATTATAGGG  
High quality sequence start: 41  
High quality sequence stop: 561.

## Location/Qualifiers

1..825

/organism="Canis familiaris"

/mol\_type="mRNA"

/db\_xref="taxon:9615"

/clone="CH3#007\_D04"

/tissue\_type="heart"

/cell\_type="heart"

/dev\_stage="mixed developmental stages (adult, 30 day - 40 day fetal)"

/clone\_lib="Canine heart normalized cDNA Library in pBluescript"

/note="Organ: heart; Vector: pBluescript; Site: 1: 5' of vector NotI; Site 2: 3' of vector EcoRI; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction: oligo-dT primed"

## ORIGIN

Query Match 42.8%; Score 257.2; DB 5; Length 825;  
Best Local Similarity 79.9%; Pred. No. 2.3e-59;  
Matches 326; Conservative 0; Mismatches 58; Indels 24; Gaps 1;

QY 1 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGTGGGATCACATGTTCACTGTTGAC 60  
|||  
Db 115 CAGCTGTGGCTACAGCTGAGTCAGAGCTGAAAGGTGGGATCACATGTTCACTGTTGAC 174  
|||  
QY 61 TTCTGGACTATTATGAAATCACACACAGCAAG----- 96  
|||  
Db 175 TTCTGGACTATTATGAAATCACACACAGCAAGTAAACGAAGCTCGGGGTATCGTCT 234  
|||  
QY 97 GAGTCCCAACCCCTCAGGTCATCTGGGCTGTGAATGCAAGAGACACAGTACCGAG 156  
|||  
Db 235 GAGTCCCAACCTCTCAAGTGTATCTGGGCTGTGAAGTCAAGAGACACAGTACCGAG 294  
|||  
QY 157 GCCTACTGGAAGTACGGGTATGATGGCAGGAGCACCTTTGAATTTCTGCCCTGCACACTG 216  
|||  
Db 295 GGGTTCTGGAAGTATGGGTATGACCGACAGAACCATCTGGAATTTCTGCCCTGAGAGCTG 354  
|||  
QY 217 GATTGGAGAGCAGAGAACCCAGGGCTTGGCCCAACCAAGCTGGAGTGGGAAAGGCAAG 276  
|||  
Db 355 GATTGGAGAGCAGGAGGCCAACAGGCCACCAAGCTGGAGTGGGAAAGTGAACAAG 414  
|||  
QY 277 ATTTCGGCCAGGCAGACACAGGGCTTACCTGGAGAGGACTGCCCTGCAGAGTACCGAG 336  
|||  
Db 415 ATTTCGGCCAGGCAGACACAGGGCTTACCTGGAGAGGAGTGTCTGAGAGGAGTGTCTG 474  
|||  
QY 337 TTCTGGAGCTGGGAGAGGAGTGTCTTGGACCAACAAAGTGCCTCTCTTTG 384  
|||  
Db 475 CTGCTGGAGCTGGGAGAGGAGGTTCTAGACCGGCAAGAGGCCGCCGATG 522  
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## RESULT 12

AI850020 457 bp mRNA linear EST 15-JUL-1999  
LOCUS AI850020



DEFINITION UI-M-BGO-aib-g-10-0-UI.s1 NIH BMAP MSC Mus musculus cDNA clone  
 ACCESSION UI-M-BGO-aib-g-10-0-UI 3', mRNA sequence.  
 VERSION AI850020  
 KEYWORDS AI850020.1 GI:5493926  
 SOURCE EST.  
 ORGANISM Mus musculus (house mouse)  
 REFERENCE 1 (bases 1 to 457)  
 AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
 JOURNAL Genom Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PUBMED 8889548  
 COMMENT Contact: Chin, H  
 National Institute of Mental Health  
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
 20892-9643, USA  
 Tel: 301 443 1706  
 Fax: 301 443 9890  
 Email: mEST@mail.nih.gov  
 Oligo-dT track not found, Not I site shown in beginning of sequence  
 is likely internal to the message. cDNA Library Preparation: M.B.  
 Soares Lab Clone distribution: NIH BMAP cDNA clones will be made  
 available by the means that is soon to be determined. When NIH  
 determines the means for distribution of the BMAP cDNA clones, this  
 record will be updated accordingly when that means is determined.  
 The following repetitive elements were found in this cDNA sequence:  
 3-30, >(CAG)n#Simple repeat  
 Seq primer: M13 Forward  
 POLYA=No.

FEATURES  
 source  
 1..457  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UI-M-BGO-aib-g-10-0-UI"  
 /dev\_stage="27-32 days"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="NIH BMAP MSC"  
 /notes="Vector: pT7T3D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; The  
 NIH BMAP MSC library is a non-normalized library  
 constructed from mouse spinal cord. The tag is a string  
 of 5 nucleotides present between the Not I site and the  
 oligo-dT track. The library was constructed as described  
 by Bonaldo, Lennon and Soares, Genome Research 6:  
 791-806, 1996. Tissue provided by Ms. Annie Novakovich,  
 Zivic-Miller Laboratories.  
 TAG\_TISSUE=spinal-cord  
 TAG\_LIB=NIH BMAP MSC  
 TAG\_SEQ=TCGAA"

ORIGIN  
 Query Match 41.8%; Score 251.4; DB 1; Length 457;  
 Best Local Similarity 79.8%; Pred. No. 7.7e-58;  
 Matches 297; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 97 GAGTCCACACCTGCAGGCTCATCTCTGGGCTGTGAATGCAAGACACAGTACCGAG 156  
 |||||  
 DB 85 GAGTCCACATCTCTGCAGGTGCTTAGCTGTGAGTGCATGAACACAGTACCAAG 144  
 |||||  
 QY 157 GGCTACTGGAAGTACGGGTATGATGGCAGGACCACTTGAATTCGCCCTGACACTG 216  
 |||||  
 DB 145 GGCTTCTGGAGATATGTTATGACGGCAAGATCACCTGGAATTCGCCCAAGACTA 204  
 |||||  
 QY 217 GATTGAGACACAGACAGCCAGGCTGCCCCACCAAGCTGAGTGGGAAGGCAAG 276  
 |||||  
 DB 205 AACTGAGCGCAGCCAGCGAGCGGCTGGGCCACCAAGTGAATGGGACGACCAAG 264  
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QY 277 ATTCTGGGCCAGGACAGACAGGGCTTACCTGGAGAGGAGTCCCTGACAGCTGCAGCAG 336  
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 DB 265 ATCCGTGCCAAACAGAACAGAGGACTACCTGGAGAGGAGTCCCTGAGCAGTGAACGG 324  
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 QY 337 TTCTCGAGCTGGGAGAGGTGTTTGGACCAACAAGTGCCTCTTTTGGTGAAGTGACA 396  
 |||||  
 DB 325 CTCTCGAGCTGGGAGAGGCGTCTCTGGGACAGCAAGTGCCTACTTTTGGTGAAGTGACT 384  
 |||||  
 QY 397 CATCATGTGACCTCTTTCAGTGACCACTCTACGGTGTGGGCTTGAACCTACTACCCCCAG 456  
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 DB 385 CGGCATGGGCTCTACGGGACCTCTCTAAGGTGTGAGGCTCTGGACTTCTTCCCCAG 444  
 |||||  
 QY 457 AACATCACCATGA 469  
 |||||  
 DB 445 AACATCACTATGA 457  
 |||||

RESULT 13  
 BE995172  
 LOCUS  
 DEFINITION UI-M-CGOp-bil-h-10-0-UI.s1 NIH BMAP Ret4\_S2 Mus musculus cDNA clone  
 UI-M-CGOp-bil-h-10-0-UI 3', mRNA sequence.  
 BE995172  
 BE995172.1 GI:10679153  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 455)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
 JOURNAL Genom Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PUBMED 8889548  
 COMMENT Contact: Chin, H  
 National Institute of Mental Health  
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
 20892-9643, USA  
 Tel: 301 443 1706  
 Fax: 301 443 9890  
 Email: mEST@mail.nih.gov  
 Oligo-dT track not found, Not I site shown in beginning of sequence  
 is likely internal to the message. cDNA Library Preparation: M.B.  
 Soares Lab Clone distribution: Researchers may obtain BMAP cDNA  
 clones from RESEARCH GENETICS. It should be noted that Bento Soares  
 is generating a small number of additional specialized  
 non-redundant arrays of BMAP cDNAs whose availability will be  
 considered under appropriate and limited collaborative arrangements  
 The tissue for this library was contributed by Dr. Xin-Yuan Fu,  
 Yale University School of Medicine The following repetitive  
 elements were found in this cDNA sequence: 1-31,  
 >(CAG)n#Simple repeat  
 Seq primer: M13 Forward  
 POLYA=No.

FEATURES  
 Location/Qualifiers  
 1..455  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UI-M-CGOp-bil-h-10-0-UI"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="NIH BMAP Ret4\_S2"  
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; The  
 NIH BMAP Ret4\_S2 library is a subtracted library.  
 ultimately derived from mouse retina tissue libraries at  
 various stages of development. For a detailed description  
 of the library from which this clone was derived, please  
 visit our web site at brainest.eng.uiowa.edu. The tissue  
 for this library was contributed by Dr. Xin-Yuan Fu, Yale



University School of Medicine  
TAG\_SEQ=None found"

ORIGIN	Query Match	41.3%;	Score 248.4;	DB 2;	Length 455;	
	Best Local Similarity	79.5%;	Pred. No. 5.1e-57;			
	Matches 294;	Conservative 0;	Mismatches 76;	Indels 0;	Gaps 0;	
QY	97	GAGTCCCAACACCTGTCAGGTCTCTCTGGGCTGTGAAATGCAAGACAAACAGTACCGAG	156			
DB	86	GAGTCCCAACATCTGTCAGGTGGTCTCTAGGCTGTGAGTGCATGAAGACAAACAGTACCGC	145			
QY	157	GCTACTGGAAGTACGGGTATGATGGCAGGACCACCTTGAATCTGCGCTGACACATG	216			
DB	146	GGCTTCTGGAGATATGGTATGACGGGCAAGATCACCTGGAATCTGCCCCAAGACACTA	205			
QY	217	GATTGGAGAGCAGCAAGAACCCAGGGCTGTGCCCCACCAAGCTGGAGTGGGAAGGCACAA	276			
DB	206	AACTGGAGCGCAGCCAGCCAGGGGCTGTGGCCACCAAGGTGGAATGGACGACACAA	265			
QY	277	ATTGGGGCCAGGCAGAACAGGGCTTACCTGGAGAGGGAATGCGCTGCAACAGTGCAGCAG	336			
DB	266	ATCCGTGCCAAACAGAACAGGACTACCTGGAGAGGACTGCGCCGAGCAGCTGAAACGG	325			
QY	337	TTCTGGAGCTGGGAGAGGTGTTTGGACCAACAGTGCCTCTTGGTGAAGTGACA	396			
DB	326	CTCCTGGAGCTGGGAGAGGCGTTCGGACAGCAAGTGCCTACTTTGGTGAAGTGACT	385			
QY	397	CATCATGTGACCTCTTTCAGTGACCACTCTACGGTGTGCGGGCTTGAACCTACTACCCCC	456			
DB	386	CGCCACTGGGCTCTACGGGACCTCTCTAAGGTGTGAGGCTCTGAGCTCTTCTCCCC	445			
QY	457	AACATCAACA 466				
DB	446	AACATCACTA 455				

RESULT 14	CA569584	542 bp	mRNA	linear	EST 19-NOV-2002
LOCUS	K0445A07-5N	NIA Mouse Mesenchymal Stem Cell cDNA Library (Long)	Mus musculus	cDNA clone NIA:K0445A07	IMAGE:30063366 5', mRNA sequence.
DEFINITION	CA569584				
ACCESSION	CA569584.1	GI:25114271			
VERSION	EST.				
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G., Umezawa, A. and Ko, M.S.H.				
AUTHORS	Systematic Analyses of NIA Mouse Mesenchymal Stem Cell cDNA Library (Long)				
TITLE	Unpublished (2001)				
JOURNAL	Other ESTs: K0445A07-3				
COMMENT	Contact: Dawood B. Dudekula Laboratory of Genetics National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@igsun.grc.nia.nih.gov Plate: K0445 row: A column: 07 Seq primer: M13 Reverse High quality sequence stop: 542 POLYA=No.				
FEATURES	Location/Qualifiers				
Source	1..542				
	/organism="Mus musculus"				
	/mol_type="mRNA"				
	/strain="C3H/He"				
	/db_xref="niaEST:K0445A07-5N"				
	/db_xref="taxon:10090"				
	/clone="NIA:K0445A07 IMAGE:30063366"				

/tissue\_type="Mesenchymal stem cell"  
/cell\_line="9-15-C cells"  
/lab\_host="DH10B"  
/clone\_lib="NIA Mouse Mesenchymal Stem Cell cDNA Library (Long)"  
[Note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11541991]. Total RNAs were obtained from Dr. Akihiro Umezawa (Keio University School of Medicine, Japan). Double-stranded cDNAs were synthesized with an oligo(dT) primer [Invitrogen: 5'-pCAGTAGTTCATGACGAGCGCGCCCTTTTITTTTITTTI-3'] from 2.2 ug of total RNA, treated with 74 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Loe-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN

Query Match	40.7%;	Score 244.6;	DB 6;	Length 542;
Best Local Similarity	76.7%;	Pred. No. 6e-56;		
Matches 323;	Conservative 0;	Mismatches 74;	Indels 24;	Gaps 1;
QY	1	CAGATGTGCTGCAGCTGAGTCAGAGTCTGAAAGGTGGGATCACATGTTCACTGTGAC	60	
DB	121	CAGCTGTGCTGCATCTGAGTCAGAGCCTGAAAGGTGGGACTACATGTTTCATAGTAGAC	180	
QY	61	TTCTGGACTATTATGGAATCACAAACACACAG------	96	
DB	181	TTCTGGACCATCATGGCAACTATAACCAAGGTACGAAGTTGGAGTGGTGTCC	240	
QY	97	GAGTCCCAACACCTGTCAGGTCTCTGGGCTGTGAAATGCAAGAACACACAGTACCGAG	156	
DB	241	GAGTCCCACTCTCTGAGGTGTCTTAGCTGTGAGTGCATGAAGACACAGTACCAGC	300	
QY	157	GGCTACTGGAAGTACGGGTATGATGGCAGGACCACTTTGAATTTGCCCCGACACACTG	216	
DB	301	GGCTTCTGGAGATATGTTATGACGGCAAGATCACCTGGAATTTCTGCCCAAGACACTA	360	
QY	217	GATTGGAGACGACAGAACCCAGGGCTGGCCCAACCAAGCTGGAGTGGGAAGGCACAG	276	
DB	361	AACTGGAGCGACCGCCAGCCAGCGGCTGGGCCACCAAGGTGGAATGGGACGAGCAAG	420	
QY	277	ATTGGGGCCAGCAGAACAGGGCTTACCTGGAGAGGGACTGCCCTGCACAGCTGCAGCAG	336	
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LOCUS  
DEFINITION  
ACCESSION  
VERSION

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PM4-ET0209-151200-003-f07 ET0209 Homo sapiens cDNA, mRNA sequence.  
BF883952  
BF883952.1 GI:12274078



**FEATURES**  
**source**

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Best Local Similarity	100.0%;	Pred. No. 5.5e-52;		
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Job time : 1900.7 secs



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 09:49:25 ; Search time 94.9625 Seconds  
(without alignments)  
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Sequence: 1 CAGATGCTGCTGAGTGTAG.....GGAAGACGAGATATACGT 601

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

Database : Issued Patents NA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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; Sequence 9, Application US/08652265  
; Patent No. 6025130  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Winston J.  
; APPLICANT: Drayna, Dennis T.  
; APPLICANT: Feder, John N.  
; APPLICANT: Gnirke, Andreas  
; APPLICANT: Ruddy, David  
; APPLICANT: Tsuchihashi, Zenta  
; APPLICANT: Wolff, Roger K.  
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,265  
; FILING DATE: 23-MAY-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 17957-000500  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1440 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
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; NAME/KEY: allele  
; LOCATION: replace (408, "c")



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QY	61	TTCTGGACTATTATPGAAAAATCAAAACAAGCAAGGAGTCCCAACCCCTGCAGGTCAATC	120	
DB	525	TTCTGGACTATTATPGAAAAATCAAAACAAGCAAGGAGTCCCAACCCCTGCAGGTCAATC	584	
QY	121	CTGGGCTGTGAATGCAAGAAAGCAACAGTACCGAGGGCTACTTGGAAAGTACGGGTATGAT	180	
DB	585	CTGGGCTGTGAATGCAAGAAAGCAACAGTACCGAGGGCTACTTGGAAAGTACGGGTATGAT	644	
QY	181	GGGCAGGACCACTTGAATTCTGCCCTTGACACACTGGATTGGAGAGCAGCAACCCAGG	240	
DB	645	GGGCAGGACCACTTGAATTCTGCCCTTGACACACTGGATTGGAGAGCAGCAACCCAGG	704	
QY	241	GCCTGGCCCAACCAAGCTGGAGTGGGAAGGCACAAAGATTGGGCCAGGCAGCAACGGGCC	300	
DB	705	GCCTGGCCCAACCAAGCTGGAGTGGGAAGGCACAAAGATTGGGCCAGGCAGCAACGGGCC	764	
QY	301	TACCTGAGAGGGACTGCCCTTGACACAGCTGCAGCAGTTGCTGGAGCTGGGAGAGGTGTT	360	
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; Sequence 10, Application US/08652265  
; Patent No. 6025130  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Winston J.  
; APPLICANT: Dravna, Dennis T.

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1 APPLICANT: Feder, John N.
2 APPLICANT: Gnirke, Andreas
3 APPLICANT: Ruddy, David
4 APPLICANT: Tsuchihashi, Zenta
5 APPLICANT: Wolff, Roger K.
6 TITLE OF INVENTION: Hereditary Hemochromatosis Gene
7 NUMBER OF SEQUENCES: 44
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Townsend and Townsend and Crew LLP
10 STREET: Two Embarcadero Center, Eighth Floor
11 CITY: San Francisco
12 STATE: California
13 COUNTRY: USA
14 ZIP: 94111-3834
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: PatentIn Release #1.0, Version #1.30
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/652,265
22 FILING DATE: 23-MAY-1996
23 CLASSIFICATION: 514
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Smith, William M.
26 REGISTRATION NUMBER: 30,223
27 REFERENCE/DOCKET NUMBER: 17957-000500
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (415) 576-0200
30 TELEFAX: (415) 576-0300
31 INFORMATION FOR SEQ ID NO: 10:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 1440 base pairs
34 TYPE: nucleic acid
35 STRANDEDNESS: single
36 TOPOLOGY: linear
37 MOLECULE TYPE: cDNA
38 FEATURE:
39 NAME/KEY: CDS
40 LOCATION: 222..1268
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QY 601 T 601  
Db 1065 T 1065

RESULT 3

US-08-652-265-11  
; Sequence 11, Application US/08652265  
; Patent No. 6025130  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Winston J.  
; APPLICANT: Drayna, Dennis T.  
; APPLICANT: Feder, John N.  
; APPLICANT: Gairke, Andreas  
; APPLICANT: Ruddy, David  
; APPLICANT: Tsuchihashi, Zenta  
; APPLICANT: Wolff, Roger K.  
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,265  
; FILING DATE: 23-MAY-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 17957-000500  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1440 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 222..1268  
; FEATURE:  
; NAME/KEY: allele

; LOCATION: replace(408, "g")  
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis"  
; OTHER INFORMATION: /label= 24d2  
US-08-652-265-11  
Query Match 100.0%; Score 601; DB 3; Length 1440;  
Best Local Similarity 100.0%; Pred. No. 2.8e-175;  
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAGATGTGCTGCAGCTGAGTCTGAAAGGGTGGGATCACAATGTTCACTGTTGAC 60  
Db 465 CAGATGTGCTGCAGCTGAGTCTGAAAGGGTGGGATCACAATGTTCACTGTTGAC 524  
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Db 1065 T 1065

RESULT 4

US-08-652-265-12  
; Sequence 12, Application US/08652265  
; Patent No. 6025130  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Winston J.  
; APPLICANT: Drayna, Dennis T.  
; APPLICANT: Feder, John N.  
; APPLICANT: Gairke, Andreas  
; APPLICANT: Ruddy, David  
; APPLICANT: Tsuchihashi, Zenta  
; APPLICANT: Wolff, Roger K.  
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco



[illegible]



STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 222..1268  
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NAME/KEY: allele  
LOCATION: replace(408, "c")  
OTHER INFORMATION: /phenotype= "normal or wild-type"  
OTHER INFORMATION: (unaffected)  
OTHER INFORMATION: /label= 24d2

FEATURE:  
NAME/KEY: allele  
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NAME/KEY: allele  
LOCATION: replace(1066, "g")  
OTHER INFORMATION: /phenotype= "normal or wild-type"  
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OTHER INFORMATION: /label= 24d1

US-08-834-497A-9

Query Match 100.0%; Score 601; DB 3; Length 1440;  
Best Local Similarity 100.0%; Pred. No. 2.8e-175; Indels 0; Gaps 0;  
Matches 601; Conservative 0; Mismatches 0;

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DB	705	GCTGCCCCACCAAGCTGAGTGGGAAAGGCAAGATTCGGGCCAGGAGAGGGCC	764
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QY 601 T 601

DB 1065 T 1065

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US-08-834-497A-10  
; Sequence 10, Application US/08834497A  
; Patent No. 6140305  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Winston J.  
; APPLICANT: Drayna, Dennis T.  
; APPLICANT: Feder, John N.  
; APPLICANT: Gnirke, Andreas  
; APPLICANT: Ruddy, David  
; APPLICANT: Teuchihaishi, Zenta  
; APPLICANT: Wolff, Roger K.  
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/834,497A  
; FILING DATE: 04-APR-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/652,265  
; FILING DATE: 23-MAY-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/632,673  
; FILING DATE: 16-APR-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/630,912  
; FILING DATE: 04-APR-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Poissant, Brian M.  
; REGISTRATION NUMBER: 28,462  
; REFERENCE/DOCKET NUMBER: 8907-0056-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1440 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 222..1268  
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; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis"  
; OTHER INFORMATION:  
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; US-08-834-497A-10

Query Match 100.0%; Score 601; DB 3; Length 1440;  
Best Local Similarity 100.0%; Pred. No. 2.8e-175;  
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;











APPLICANT: Drayna, Dennis T.  
 APPLICANT: Feder, John N.  
 APPLICANT: Gnirke, Andreas  
 APPLICANT: Ruddy, David  
 APPLICANT: Teuchihaashi, Zenta  
 APPLICANT: Wolff, Roger K.  
 TITLE OF INVENTION: Hereditary Hemochromatosis Gene  
 NUMBER OF SEQUENCES: 44  
 CORRESPONDENCE ADDRESS:  
 ADDRESSES: Pennie & Edmonds LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: Windows 95  
 SOFTWARE: WordPerfect Version 8  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/503,444A  
 FILING DATE: 14-Feb-2000  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/652,265  
 FILING DATE: 23-May-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/632,673  
 FILING DATE: 16-Apr-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/630,912  
 FILING DATE: 04-Apr-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Poissant, Brian M.  
 REGISTRATION NUMBER: 28,462  
 REFERENCE/DOCKET NUMBER: 8907-0088-999  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-790-9090  
 TELEFAX: 212-869-9741  
 TELEX: 66141  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1440 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 222..1268  
 FEATURE:  
 NAME/KEY: allele  
 LOCATION: replace(408, "c")  
 OTHER INFORMATION: /phenotype= "normal or wild-type"  
 OTHER INFORMATION: (unaffected)  
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 NAME/KEY: allele  
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 OTHER INFORMATION: /phenotype= "normal or wild-type"  
 OTHER INFORMATION: (unaffected)  
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 FEATURE:  
 NAME/KEY: allele  
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 OTHER INFORMATION: /phenotype= "normal or wild-type"  
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Query Match 100.0%; Score 601; DB 3; Length 1440;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-175;

Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CAGATGTGGCTGCAGCTCAGTCTGAGTCTGAAAGGGTGGGATCAATGTTCACTGTTGAC 60  
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 QY 61 TTCTGGACTATTATGGAATAACACCAACCAAGCAGGAGTCCACACCTCGCAGGTCAATC 120  
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 ; Sequence 10, Application US/09503444A  
 ; Patent No. 6228594  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Thomas, Winston J.  
 ; APPLICANT: Drayna, Dennis T.  
 ; APPLICANT: Feder, John N.  
 ; APPLICANT: Gnirke, Andreas  
 ; APPLICANT: Ruddy, David  
 ; APPLICANT: Teuchihaashi, Zenta  
 ; APPLICANT: Wolff, Roger K.  
 ; TITLE OF INVENTION: Hereditary Hemochromatosis Gene  
 ; NUMBER OF SEQUENCES: 44  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSES: Pennie & Edmonds LLP  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: Windows 95  
 ; SOFTWARE: WordPerfect Version 8



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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,444A
; FILING DATE: 14-Feb-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/652,265
; FILING DATE: 23-May-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,673
; FILING DATE: 16-Apr-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,912
; FILING DATE: 04-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0088-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 222..1268
; FEATURE:
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; LOCATION: replace(1066, "a")
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis"
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US-09-503-444A-10

Query Match 100.0%; Score 601; DB 3; Length 1440;
Best Local Similarity 100.0%; Pred. No. 2.8e-175; Mismatches 0; Indels 0; Gaps 0;
Matches 601; Conservative 0;

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DB 585 CTGGGCTGTGAATGCAAGAGACACAGTACCAGGGCTACTGGAAGTACGGGTATGAT 644
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RESULT 11
US-09-503-444A-11
; Sequence 11, Application US/09503444A
; Patent No. 6228594
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect Version 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,444A
; FILING DATE: 14-Feb-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/652,265
; FILING DATE: 23-May-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,673
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,912
; FILING DATE: 04-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
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; REFERENCE/DOCKET NUMBER: 8907-0088-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 222..1268
; FEATURE:
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; NAME/KEY: allele
; LOCATION: replace(408, "g")
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis"
; OTHER INFORMATION: /label= 24d2
; US-09-503-444A-11

Query Match      100.0%; Score 601; DB 3; Length 1440;
Best Local Similarity 100.0%; Pred. No. 2.8e-175;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGATCACAATGTTCACTGTTGAC 60
DB 465 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGATCACAATGTTCACTGTTGAC 524
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DB 525 TTCTGGACTATTATGAAATCACAACCAACAGCAAGAGTCCCAACCCCTGCAGGTCAATC 584
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RESULT 12
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; Sequence 12, Application US/09503444A
; Patent No. 6228594
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
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; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect Version 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,444A
; FILING DATE: 14-Feb-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/652,265
; FILING DATE: 23-May-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,673
; FILING DATE: 16-Apr-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,912
; FILING DATE: 04-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0088-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 222..1268
; FEATURE:
; NAME/KEY: allele
; LOCATION: replace(408, "g")
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis"
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DB 645 GGGCAGGACCACTTGAATTTCTGCCCTGCACACTGGATTGGAGAGCAGCAGAACCCAGG 704
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RESULT 13
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; Patent No. 6355425
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Barry E.
; APPLICANT: Sawada-Hirai, Ritsuko
; APPLICANT: Barton, James C.
; TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
; FILE REFERENCE: 10653/002001
; CURRENT APPLICATION NUMBER: US/09/277,457
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2506
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (0)...(0)
; OTHER INFORMATION: Missense mutation at nucleotide 314
US-09-277-457-1

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Db	664	ACTCTACGGTTCGGGGCTTGAACCTACTACTACCCCAAGAACATCACCATGAAGTGGCTGAAG	723
QY	481	GATTAAGCAGCAATGGATGCCAAAGGAGTTCGAACTCTAAAGACGTATTGCCCAATGGGGAT	540
Db	724	GATTAAGCAGCAATGGATGCCAAAGGAGTTCGAACTCTAAAGACGTATTGCCCAATGGGGAT	783
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; Patent NO. 6509442
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, Barry E.
; APPLICANT: Sawada-Hirai, Ritsuko
; APPLICANT: Barton, James C.
; TITLE OF INVENTION: MUTATIONS ASSOCIATED WITH IRON DISORDERS
; FILE REFERENCE: 24065-004 DIV
; CURRENT APPLICATION NUMBER: US/09/679,729
; CURRENT FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 09/277,457
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2506
; TYPE: DNA
; ORGANISM: Homo Sapiens
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; NAME/KEY: mutation
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US-09-679-729-1

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Db 844 T 844
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; Sequence 1180, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
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; NUMBER OF SEQ ID NOS: 207012
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US-09-949-016-1180
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Best Local Similarity 100.0%; Pred. No. 4e-175;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 121 CTGGGCTGTGAATGCAAGAACACACAGTACCGAGGGCTACTGGAAAGTACCGGTATGAT 180
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Qy 481 GATAAGCAGCCAATGATGCCAAGGAGTTTCGAACCTTAAAGACGTATTGCCCAATGGGGAT 540
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GenCore version 5.1.6  
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OM nucleic-- nucleic search, using sw model

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SUMMARIES

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4	601	100.0	1440	15	US-10-138-888-12
5	601	100.0	1440	15	US-10-138-888-77
6	601	100.0	2506	10	US-09-981-606-1
7	601	100.0	2739	21	US-10-956-250-1

Sequence 271, App	2285	21	US-10-741-600-271
Sequence 269, App	2426	21	US-10-741-600-269
Sequence 265, App	2716	21	US-10-741-600-265
Sequence 267, App	2674	21	US-10-741-600-267
Sequence 264, App	2231	21	US-10-741-600-264
Sequence 268, App	2189	21	US-10-741-600-268
Sequence 23829, A	282	16	US-10-029-386-23829
Sequence 10129, A	500	16	US-10-029-386-10129
Sequence 3112, Ap	5749	9	US-09-764-877-3112
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Sequence 1, Appl	235033	15	US-10-301-844-1
Sequence 2, Appl	237326	15	US-10-301-844-2
Sequence 17631, A	21608	21	US-10-741-600-17631
Sequence 105, App	596	17	US-10-158-057-105
Sequence 21, Appl	517	15	US-10-138-888-20
Sequence 21, Appl	517	15	US-10-138-888-21
Sequence 266, App	2009	21	US-10-741-600-266
Sequence 261, App	2440	21	US-10-741-600-261
Sequence 263, App	1955	21	US-10-741-600-263
Sequence 7420, Ap	201	21	US-10-741-600-7420
Sequence 7429, Ap	201	21	US-10-741-600-7429
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Sequence 7503, Ap	201	21	US-10-741-600-7503

ALIGNMENTS

RESULT 1

US-10-138-888-9  
; Sequence 9, Application US/10138888  
; Publication No. US20030148972A1  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Winston J.  
; Drayna, Dennis T.  
; Feder, John N.  
; Gnirke, Andreas  
; Ruddy, David  
; Tsuchihashi, Zenta  
; Wolff, Roger K.  
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene  
; NUMBER OF SEQUENCES: 79  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/10/138,888  
; APPLICATION NUMBER: US/10/138,888  
; FILING DATE: 02-May-2002  
; CLASSIFICATION: <Unknown>







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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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  LOCATION: 222..1268
FEATURE:
  NAME/KEY: allele
  LOCATION: replace(1066, "a")
  OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
(HH)"
/label= 24d1
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-138-888-10

Query Match      100.0%; Score 601; DB 15; Length 1440;
Best Local Similarity 100.0%; Pred. No. 5.8e-184;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGATGTGGCTGCAGCTGAGTCAAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 60
DB 465 CAGATGTGGCTGCAGCTGAGTCAAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 524
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; Publication No. US20030148972A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; Drayna, Dennis T.
; Feder, John N.
; Gnirke, Andreas
```

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; Ruddy, David
; Tsuchihashi, Zenta
; Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; SOFTWARE: Patentin Release #1.0, Version #1.30
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; FILING DATE: 02-May-2002
; CLASSIFICATION: <Unknown>
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; FILING DATE: 04-APR-1997
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brian M. Poissant
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-095-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 222..1268
; FEATURE:
; NAME/KEY: allele
; LOCATION: replace(408, "g")
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
(HH)"
/label= 24d2
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-138-888-11

Query Match      100.0%; Score 601; DB 15; Length 1440;
Best Local Similarity 100.0%; Pred. No. 5.8e-184;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGATGTGGCTGCAGCTGAGTCAAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 60
DB 465 CAGATGTGGCTGCAGCTGAGTCAAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 524
QY 61 TTCTGGACTATTATGGAATAATCAACACAGCAAGAGTCCACACCCCTGCAGGTCATC 120
DB 525 TTCTGGACTATTATGGAATAATCAACACAGCAAGAGTCCACACCCCTGCAGGTCATC 584
QY 121 CTGGGCTGTGAATGCAAGAAGCAACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 180
DB 585 CTGGGCTGTGAATGCAAGAAGCAACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 644
QY 181 GGGCAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAGG 240
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Db 645 GGGAGGACCACTTGAATTCGCCCTGACACACTGGATTGGAGAGCAGAGAACCCAGG 704
Qy 241 GCCTGGCCCAACAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGAGAACAGGGCC 300
Db 705 GCCTGGCCCAACAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGAGAACAGGGCC 764
Qy 301 TACCTGGAGAGGACTGCGCTTGCACAGCTGCGAGAGTTCCTGGAGTGGGGAGAGGTGTT 360
Db 765 TACCTGGAGAGGACTGCGCTTGCACAGCTGCGAGAGTTCCTGGAGTGGGGAGAGGTGTT 824
Qy 361 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 420
Db 825 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 884
Qy 421 ACTTACCGTGTGGGCCCTTGAACCTACTACCCCGAGAACATCACCATTGAAGTGGCTGAAG 480
Db 885 ACTTACCGTGTGGGCCCTTGAACCTACTACCCCGAGAACATCACCATTGAAGTGGCTGAAG 944
Qy 481 GATAAGCAGCCAAATGATGCCAAGGAGTTGGAACCTTAAAGAGCTATTGCCCAATGGGGAT 540
Db 945 GATAAGCAGCCAAATGATGCCAAGGAGTTGGAACCTTAAAGAGCTATTGCCCAATGGGGAT 1004
Qy 541 GGGACCTACAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACG 600
Db 1005 GGGACCTACAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACG 1064
Qy 601 T 601
Db 1065 T 1065
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RESULT 4

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US-10-138-888-12
; Sequence 12, Application US/1013888
; Publication No. US20030148972A1
; GENERAL INFORMATION:
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APPLICANT: Thomas, Winston J.
           Drayna, Dennis T.
           Feder, John N.
           Gnirke, Andreas
           Ruddy, David
           Teuchihashi, Zenta
           Wolff, Roger K.
```

TITLE OF INVENTION: Hereditary Hemochromatosis Gene

NUMBER OF SEQUENCES: 79

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/138,888

FILING DATE: 02-May-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/834,497

FILING DATE: 04-APR-1997

APPLICATION NUMBER: US 08/652,265

FILING DATE: 23-MAY-1996

APPLICATION NUMBER: US 08/632,673

FILING DATE: 16-APR-1996

APPLICATION NUMBER: US 08/630,912

FILING DATE: 04-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Brian M. Poissant

```
;
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-095-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 222..1268
; FEATURE:
; NAME/KEY: allele
; LOCATION: replace(1066, "a")
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
; (HH) "
; /label= 24d2
; FEATURE:
; NAME/KEY: allele
; LOCATION: replace(1066, "a")
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
; (HH) "
; /label= 24d1
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
;
US-10-138-888-12
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Query Match 100.0%; Score 601; DB 15; Length 1440;
Best Local Similarity 100.0%; Pred. No. 5.8e-184;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCAGATGTTCACTGTTGAC 60
Db 465 CAGATGTGGCTGCAGCTGAGTCAGAGTCTGAAAGGGTGGGATCAGATGTTCACTGTTGAC 524
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Db 525 TTCTGGACTATTATGGAATAATCAACCAAGCAAGAGGATGCCACACCTTCAGGTCATC 584
Qy 121 CTGGGCTGTGAATGCAAGAGACACAGTACCGAGGGCTACTTGGAGTTCGAGAGCAGAGCCAGG 180
Db 585 CTGGGCTGTGAATGCAAGAGACACAGTACCGAGGGCTACTTGGAGTTCGAGAGTTCGAGTATGAT 644
Qy 181 GGGCAGGACCACTTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGAGAACCCAGG 240
Db 645 GGGCAGGACCACTTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGAGAACCCAGG 704
Qy 241 GCCTGGCCCAACAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGAGAACAGGGCC 300
Db 705 GCCTGGCCCAACAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGAGAACAGGGCC 764
Qy 301 TACCTGGAGAGGACTGCGCTTGCACAGCTGCGAGAGTTCCTGGAGTGGGGAGAGGTGTT 360
Db 765 TACCTGGAGAGGACTGCGCTTGCACAGCTGCGAGAGTTCCTGGAGTGGGGAGAGGTGTT 824
Qy 361 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 420
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Db 885 ACTTACCGTGTGGGCCCTTGAACCTACTACCCCGAGAACATCACCATTGAAGTGGCTGAAG 944
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Qy      601 T 601
Db      1065 T 1065

RESULT 5
US-10-138-888-77
; Sequence 77, Application US/10138888
; Publication No. US20030148972A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
;           Drayna, Dennis T.
;           Feder, John N.
;           Gnirke, Andreas
;           Ruddy, David
;           Tsuchihashi, Zenta
;           Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/138,888
; FILING DATE: 02-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/834,497
; FILING DATE: 04-APR-1997
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brian M. Poissant
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-095-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1440 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 222..1268
; FEATURE:
; NAME/KEY: allele
; LOCATION: replace(414, "c").
; OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis
; (HH)"
; /label= 24d7
; SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-10-138-888-77

Query Match      100.0%; Score 601; DB 15; Length 1440;
Best Local Similarity 100.0%; Pred. No. 5.8e-184;
Matches 601; Gaps 0;

Qy      601 T 601
Db      1065 T 1065

Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 TTCTGGACTATTATGGAAATCAACACAGCAAGGAGTCCACACACCTTGCAGGTGATC 120
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Qy      525 TTCTGGACTATTATGGAAATCAACACAGCAAGGAGTCCACACACCTTGCAGGTGATC 584
Db      525 TTCTGGACTATTATGGAAATCAACACAGCAAGGAGTCCACACACCTTGCAGGTGATC 584
Qy      121 CTGGGCTGTGAAATGCAAGAGACACAGTACCGAGGGCTACTTGGAAAGTACGGGTATGAT 180
Db      121 CTGGGCTGTGAAATGCAAGAGACACAGTACCGAGGGCTACTTGGAAAGTACGGGTATGAT 180
Qy      585 CTGGGCTGTGAAATGCAAGAGAGACACAGTACCGAGGGCTACTTGGAAAGTACGGGTATGAT 644
Db      585 CTGGGCTGTGAAATGCAAGAGAGACACAGTACCGAGGGCTACTTGGAAAGTACGGGTATGAT 644
Qy      181 GGGCAGGACCACTTGAATTTCTGCCCTGCACACTGATTTGGAGAGCAGCAGAACCCAGG 240
Db      181 GGGCAGGACCACTTGAATTTCTGCCCTGCACACTGATTTGGAGAGCAGCAGAACCCAGG 240
Qy      645 GGGCAGGACCACTTGAATTTCTGCCCTGCACACTGATTTGGAGAGCAGCAGAACCCAGG 704
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Qy      241 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAACAAGATTTCGGGCCAGGCAGAACAGGGCC 300
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Qy      705 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAACAAGATTTCGGGCCAGGCAGAACAGGGCC 764
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Qy      301 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGAGTTCGCTGGAGCTGGGGAGAGGTGTT 360
Db      301 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGAGTTCGCTGGAGCTGGGGAGAGGTGTT 360
Qy      765 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGAGTTCGCTGGAGCTGGGGAGAGGTGTT 824
Db      765 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGAGTTCGCTGGAGCTGGGGAGAGGTGTT 824
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Db      825 TTGGACCAACAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACCTCTTCAGTGAAC 884
Qy      421 ACTCTACGGTGTGGGCCCTTGAACACTACTACCCCAAGACATCACCATTGAAGTGGCTGAAG 480
Db      421 ACTCTACGGTGTGGGCCCTTGAACACTACTACCCCAAGACATCACCATTGAAGTGGCTGAAG 480
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Qy      481 GATAACGACCAATGATGCGAAGGATTCGAACCTTGAACCTTATTCGCCAATGGGGAT 540
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Db      945 GATAACGACCAATGATGCGAAGGATTCGAACCTTGAACCTTATTCGCCAATGGGGAT 1004
Qy      541 GGGACCTACAGGGCTGGATAACCTTTGGCTGTACCCCTGGGGAAGAGCAGATATACG 600
Db      541 GGGACCTACAGGGCTGGATAACCTTTGGCTGTACCCCTGGGGAAGAGCAGATATACG 600
Qy      1005 GGGACCTACAGGGCTGGATAACCTTTGGCTGTACCCCTGGGGAAGAGCAGATATACG 1064
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Qy      601 T 601
Db      1065 T 1065

RESULT 6
US-09-981-606-1
; Sequence 1, Application US/09981606
; Publication No. US20030129595A1
; GENERAL INFORMATION:
; APPLICANT: Rothenberg et al.
; TITLE OF INVENTION: Mutations associated with iron disorders
; FILE REFERENCE: 24065-004CON
; CURRENT APPLICATION NUMBER: US/09/981,606
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 09/277,457
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2506
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-981-606-1

Query Match      100.0%; Score 601; DB 10; Length 2506;
Best Local Similarity 100.0%; Pred. No. 7.1e-184;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 244 CAGATGTGGCTGAGTGCAGAGTCTGAAAGGGTGGGATCATCATGTTCACTGTTGAC 303  
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QY 121 CTGGCTGTGAATGCAAGACACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 180  
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QY 181 GGGCAGGACACCTTGAATTCCTGCTGACACACTGGATTGGAGAGCAGACAGGCCAGG 240  
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QY 241 GCTGGCCACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGACAGAGGCC 300  
Db 484 GCTGGCCACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGACAGAGGCC 543  
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QY 361 TTGGACCAACAGTGCCTCTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 420  
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Db 664 ACTCTACGGTGTGGGCCCTTGAACACTACTACCCCGAGAACATCACCATGAAGTGGCTGAAG 723  
QY 481 GATAAGCAGCCTAGTGCAGAGGTTGCAACCTTAAAGAGTATTGCCCAATGGGGAT 540  
Db 724 GATAAGCAGCCTAGTGCAGAGGTTGCAACCTTAAAGAGTATTGCCCAATGGGGAT 783  
QY 541 GGGACCTACAGGGCTGGATTAACCTTGGCTGTACCCCTGGGGAAGAGAGATATACG 600  
Db 784 GGGACCTACAGGGCTGGATTAACCTTGGCTGTACCCCTGGGGAAGAGAGATATACG 843  
QY 601 T 601  
Db 844 T 844

RESULT 7  
US-10-956-250-1  
; Sequence 1, Application US/10956250  
; Publication No. US20050090430A1  
; GENERAL INFORMATION:  
; APPLICANT: Feder, John N.  
;           Schatzman, Randall C.  
;           Tsuchihashi, Zenta  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
;           DIAGNOSIS AND TREATMENT OF IRON MISREGULATION D  
;           ISEASES  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
;           ADDRESS: Pennie & Edmonds LLP  
;           STREET: 1155 Avenue of the Americas  
;           CITY: New York  
;           STATE: NY  
;           COUNTRY: USA  
;           ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
;           MEDIUM TYPE: Diskette  
;           OPERATING SYSTEM: Windows  
;           SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
;           APPLICATION NUMBER: US/10/956,250  
;           FILING DATE: 01-Oct-2004  
;           CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
;           APPLICATION NUMBER: US/08/920,559

; FILING DATE: 27-Aug-1997  
; APPLICATION NUMBER: US 08/652,265  
; FILING DATE: 23-MAY-1996  
; APPLICATION NUMBER: US 08/834,497  
; FILING DATE: 04-APR-1997  
; APPLICATION NUMBER: US 08/866,211  
; FILING DATE: 13-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
;           NAME: Poissant, Brian M  
;           REGISTRATION NUMBER: 28,462  
;           REFERENCE/DOCKET NUMBER: 8907-0062-999  
;           TELECOMMUNICATION INFORMATION:  
;           TELEPHONE: 650-493-4935  
;           TELEFAX: 650-493-5556  
;           TELEX: 66141 PENNIE  
;           INFORMATION FOR SEQ ID NO: 1:  
;           SEQUENCE CHARACTERISTICS:  
;           LENGTH: 2739 base pairs  
;           TYPE: nucleic acid  
;           STRANDEDNESS: single  
;           TOPOLOGY: linear  
;           SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
; US-10-956-250-1  
;           Query Match           100.0%;   Score 601;   DB 21;   Length 2739;  
;           Best Local Similarity   100.0%;   Pred. No. 7.3e-184;  
;           Matches 601;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;  
QY 1 CAGATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 60  
Db 477 CAGATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCACATGTTCACTGTTGAC 536  
QY 61 TTCTGGAATTTATGAAATCAACACAGCAGAGGATCCACACCTTCAGGTGATC 120  
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QY 241 GCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAACAGATTCGGGCCAGGACAGAGGCC 300  
Db 717 GCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAACAGATTCGGGCCAGGACAGAGGCC 776  
QY 301 TACCTGGAGAGGAGTGCCTTCACAGCTGCAGCAGTTCCTGGAGCTGGGAGAGGTGT 360  
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QY 361 TTGGACCAACAGTGCCTCTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 420  
Db 837 TTGGACCAACAGTGCCTCTTGGTGAAGGTGACACATCATGTGACCTTTCAGTGACC 896  
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QY 481 GATAAGCAGCCTAGTGCAGAGTTCGAAACCTTAAAGAGTATTGCCCAATGGGGAT 540  
Db 957 GATAAGCAGCCTAGTGCAGAGTTCGAAACCTTAAAGAGTATTGCCCAATGGGGAT 1016  
QY 541 GGGACCTACAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGAGATATACG 600  
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QY 601 T 601  
Db 1077 T 1077



RESULT 8  
US-10-741-600-271  
; Sequence 271, Application US/10741600  
; Publication No. US20050026169A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001499  
; CURRENT APPLICATION NUMBER: US/10/741,600  
; NUMBER OF SEQ ID NOS: 2003-12-22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 271  
; LENGTH: 2285  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-741-600-271

Query Match 99.7%; Score 599; DB 21; Length 2285;  
Best Local Similarity 99.2%; Pred. No. 3e-183;  
Matches 596; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
  
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QY 361 TTGGACCAACAAGTGCTCTTGTGTAAGGTGACACATCATGTGACCTTTCAGTGAAC 420  
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DB 945 GATAAGCAGCAATGATGCAAGGATTCGAACCTTAAAGAGCTATTGCCCCTAAATGGGAT 1004  
  
QY 541 GGGACCTACAGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACG 600  
DB 1005 GGGACCTACAGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACG 1064  
  
QY 601 T 601  
DB 1065 T 1065

RESULT 9  
US-10-741-600-269  
; Sequence 269, Application US/10741600  
; Publication No. US20050026169A1  
; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001499  
; CURRENT APPLICATION NUMBER: US/10/741,600  
; NUMBER OF SEQ ID NOS: 2003-12-22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 269  
; LENGTH: 2426  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-741-600-269

Query Match 99.7%; Score 599; DB 21; Length 2426;  
Best Local Similarity 99.2%; Pred. No. 3.1e-183;  
Matches 596; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CAGATGTGGCTGCAGTGTGAGTCTGAAAGGCTGGGATCACATGTTCACTGTGAC 60  
DB 175 CAGATGTGGCTGCAGTGTGAGTCTGAAAGGCTGGGATCACATGTTCACTGTGAC 234  
  
QY 61 TTCTGGACTATTATGAAATCAACACACAGCAGAGGTCCACACCTTGCAGTGCATC 120  
DB 235 TTCTGGACTATTATGAAATCAACACACAGCAGAGGTCCACACCTTGCAGTGCATC 294  
  
QY 121 CTGGGCTGTGAATGCAAGAACACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 180  
DB 295 CTGGGCTGTGAATGCAAGAACACAGTACCGAGGCTACTGGAAGTACGGGTATGAT 354  
  
QY 181 GGGCAGGACACCTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGAACCCAGG 240  
DB 355 GGGCAGGACACCTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGAACCCAGG 414  
  
QY 241 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCTGGGAGAGGTGT 300  
DB 415 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCTGGGAGAGGTGT 474  
  
QY 301 TACCTGGAGAGGACTGCGCTTGTGTAAGGTGACACATCATGTGACCTTTCAGTGAAC 360  
DB 475 TACCTGGAGAGGACTGCGCTTGTGTAAGGTGACACATCATGTGACCTTTCAGTGAAC 534  
  
QY 361 TTGGACCAACAAGTGCTCTTGTGTAAGGTGACACATCATGTGACCTTTCAGTGAAC 420  
DB 535 TTGGACCAACAAGTGCTCTTGTGTAAGGTGACACATCATGTGACCTTTCAGTGAAC 594  
  
QY 421 ACTCTAGGTGTGGGCTTGAACCTTGTGTAAGGTGACACATCATGTGACCTTTCAGTGAAC 480  
DB 595 ACTCTAGGTGTGGGCTTGAACCTTGTGTAAGGTGACACATCATGTGACCTTTCAGTGAAC 654  
  
QY 481 GATAAGCAGCAATGATGCAAGGATTCGAACCTTAAAGAGCTATTGCCCCTAAATGGGAT 540  
DB 655 GATAAGCAGCAATGATGCAAGGATTCGAACCTTAAAGAGCTATTGCCCCTAAATGGGAT 714  
  
QY 541 GGGACCTACAGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACG 600  
DB 715 GGGACCTACAGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGCAGAGATATACG 774  
  
QY 601 T 601  
DB 775 T 775

RESULT 10  
US-10-741-600-265  
; Sequence 265, Application US/10741600  
; Publication No. US20050026169A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001499  
; CURRENT APPLICATION NUMBER: US/10/741,600



```
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 265
; LENGTH: 2716
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-265

Query Match      99.7%; Score 599; DB 21; Length 2716;
Best Local Similarity 99.2%; Pred. No. 3.2e-183;
Matches 596; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCAGATGTTCACTTTGAC 60
DB 465 CAGATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCAGATGTTCACTTTGAC 524

QY 61 TTCTGGACTATTATGGAATAACACAAACACAGAGAGTCCACACCTCGCAGGTCAATC 120
DB 525 TTCTGGACTATTATGGAATAACACAAACACAGAGAGTCCACACCTCGCAGGTCAATC 584

QY 121 CTGGGCTGTGAATGCAAGAGACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180
DB 585 CTGGGCTGTGAATGCAAGAGACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 644

QY 181 GGGCAGGACCACTTGAATTTGCTCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAGG 240
DB 645 GGGCAGGACCACTTGAATTTGCTCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAGG 704

QY 241 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAAGACAGGGCC 300
DB 705 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAAGACAGGGCC 764

QY 301 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTTCGCTGGAGCTGGGGAGAGGTGT 360
DB 765 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTTCGCTGGAGCTGGGGAGAGGTGT 824

QY 361 TTGGACCAACAAAGTGCCTCTTGGTGAAGGTGACACATCATGTGACCTTTCACTGACC 420
DB 825 TTGGACCAACAAAGTGCCTCTTGGTGAAGGTGACACATCATGTGACCTTTCACTGACC 480

QY 421 ACTCTACGGTGTGGGCCCTTGAATCTACTACCCCAAGACATCACCATGAAGTGGCTGAAG 480
DB 885 ACTCTACGGTGTGGGCCCTTGAATCTACTACCCCAAGACATCACCATGAAGTGGCTGAAG 944

QY 481 GATAAGCAGCAATGGATGCCAAGAGTTCGAACTTAAAGACGTAATGCCCCAATGGGGAT 540
DB 945 GATAAGCAGCAATGGATGCCAAGAGTTCGAACTTAAAGACGTAATGCCCCAATGGGGAT 1004

QY 541 GGGACCTACAGGCTGGATTAACCTTGGCTGTACCCCTGGGGAGAGCAGAGATATACG 600
DB 1005 GGGACCTACAGGCTGGATTAACCTTGGCTGTACCCCTGGGGAGAGCAGAGATATAYG 1064

QY 601 T 601
DB 1065 T 1065

RESULT 11
US-10-741-600-267
; Sequence 267, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 267
; LENGTH: 2674
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-267

Query Match      84.0%; Score 505; DB 21; Length 2674;
Best Local Similarity 92.2%; Pred. No. 9.8e-153;
Matches 554; Conservative 5; Mismatches 0; Indels 42; Gaps 1;

QY 1 CAGATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCAGATGTTCACTTTGAC 60
DB 465 CAGATGTGGCTGCAGCTGAGTCTGAAAGGGTGGGATCAGATGTTCACTTTGAC 524

QY 61 TTCTGGACTATTATGGAATAACACAAACACAGAGAGTCCACACCTCGCAGGTCAATC 120
DB 525 TTCTGGACTATTATGGAATAACACAAACACAGAGAGTCCACACCTCGCAGGTCAATC 584

QY 121 CTGGGCTGTGAATGCAAGAGACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 180
DB 585 CTGGGCTGTGAATGCAAGAGACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGAT 644

QY 181 GGGCAGGACCACTTGAATTTGCTCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAGG 240
DB 645 GGGCAGGACCACTTGAATTTGCTCCCTGACACACTGGATTGGAGAGCAGCAGAACCCAGG 704

QY 241 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAAGACAGGGCC 300
DB 705 GCCTGGCCCAACCAAGCTGGAGTGGGAAAGGCAAGATTTCGGGCCAGGCAAGACAGGGCC 764

QY 301 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTTCGCTGGAGCTGGGGAGAGGTGT 360
DB 765 TACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTTCGCTGGAGCTGGGGAGAGGTGT 824

QY 361 TTGGACCAACAAAGTGCCTCTTGGTGAAGGTGACACATCATGTGACCTTTCACTGACC 420
DB 825 TTGGACCAACAAAGTGCCTCTTGGTGAAGGTGACACATCATGTGACCTTTCACTGACC 480

QY 421 ACTCTACGGTGTGGGCCCTTGAATCTACTACCCCAAGACATCACCATGAAGTGGCTGAAG 480
DB 843 ACTCTACGGTGTGGGCCCTTGAATCTACTACCCCAAGACATCACCATGAAGTGGCTGAAG 902

QY 481 GATAAGCAGCAATGGATGCCAAGAGTTCGAACTTAAAGACGTAATGCCCCAATGGGGAT 540
DB 903 GATAAGCAGCAATGGATGCCAAGAGTTCGAACTTAAAGACGTAATGCCCCAATGGGGAT 962

QY 541 GGGACCTACAGGCTGGATTAACCTTGGCTGTACCCCTGGGGAGAGCAGAGATATACG 600
DB 963 GGGACCTACAGGCTGGATTAACCTTGGCTGTACCCCTGGGGAGAGCAGAGATATAYG 1022

QY 601 T 601
DB 1023 T 1023

RESULT 12
US-10-741-600-264
; Sequence 264, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 264
; LENGTH: 2231
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-264

Query Match      83.7%; Score 502.8; DB 21; Length 2231;
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QY 277 ATTGGGGCAGCAGACAGGGCCCTACCTGGAGAGGACTGCCCTGCACAGCTGCAGCAG 336  
|||  
Db 181 ATTGGGGCAGCAGACAGGGCCCTACCTGGAGAGGACTGCCCTGCACAGCTGCAGCAG 240  
|||  
QY 337 TTGCTGGAGCTGGGAGAGGTGTTTGGACCAACAAG 373  
|||  
Db 241 TTGCTGGAGCTGGGAGAGGTGTTTGGACCAACAAG 277  
|||

## RESULT 15

US-10-029-386-10129  
; Sequence 10129, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
; FILE REFERENCE: AEMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 10129  
; LENGTH: 500  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR6.3  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6  
; OTHER INFORMATION: NT HIT: U91328.1, EVALUE 0.00e+00  
; OTHER INFORMATION: SWISSPROT HIT: Q30201, EVALUE 1.00e-52  
; OTHER INFORMATION: EST\_HUMAN HIT: BG747345.1, EVALUE 0.00e+00  
US-10-029-386-10129

Query Match 46.1%; Score 277; DB 16; Length 500;  
Best Local Similarity 100.0%; Pred. No. 4.6e-79;  
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 97 GAGTCCACACCCCTGCAGGTCACTCTGGGCTGTGAAATGCAAGAAGACACAGTACCGAG 156  
|||  
Db 106 GAGTCCACACCCCTGCAGGTCACTCTGGGCTGTGAAATGCAAGAAGACACAGTACCGAG 165  
|||  
QY 157 GGCTACTGGAAGTACGGGTATGATGGGAGGACACCTTTGAATTTCTGCCCTGACACACTG 216  
|||  
Db 166 GGCTACTGGAAGTACGGGTATGATGGGAGGACACCTTTGAATTTCTGCCCTGACACACTG 225  
|||  
QY 217 GATTGGAGAGCAGCAGAACCCAGGGGCTTGCCCCCACCACCAAGCTGGAGTGGGAAAGGCACAAG 276  
|||  
Db 226 GATTGGAGAGCAGCAGAACCCAGGGGCTTGCCCCCACCACCAAGCTGGAGTGGGAAAGGCACAAG 285  
|||  
QY 277 ATTGGGGCCAGCAGACAGGGCCCTACCTGGAGAGGAGTGCCTTGCACAGCTGCAGCAG 336  
|||  
Db 286 ATTGGGGCCAGCAGACAGGGCCCTACCTGGAGAGGAGTGCCTTGCACAGCTGCAGCAG 345  
|||  
QY 337 TTGCTGGAGCTGGGAGAGGTGTTTGGACCAACAAG 373  
|||  
Db 346 TTGCTGGAGCTGGGAGAGGTGTTTGGACCAACAAG 382  
|||

Search completed: June 23, 2005, 06:38:40  
Job time : 349.016 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 05:24:18 ; Search time 21352.4 Seconds  
(without alignments)  
11346.531 Million cell updates/sec

Title: US-09-497-957-1\_COPY\_1\_5000  
Perfect score: 5000  
Sequence: 1 TCTAAGGTTGAGATAAAATT.....GCTAATTGGAAGCTGAGGC 5000

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5000	100.0	10825	6	AR117789 Sequence
2	5000	100.0	10825	6	AR117790 Sequence
3	5000	100.0	10825	6	AR149459 Sequence
4	5000	100.0	10825	6	AR149460 Sequence
5	5000	100.0	246240	6	AR036572 Sequence
6	5000	100.0	246240	6	AR036573 Sequence
7	5000	100.0	246240	6	AR036574 Sequence
8	4998.4	100.0	10825	6	AR117791 Sequence
9	4998.4	100.0	10825	6	AR117792 Sequence
10	4998.4	100.0	10825	6	AR149461 Sequence
11	4998.4	100.0	10825	6	AR149462 Sequence
12	4988	99.8	235033	6	BD084121 Polymorph
13	4988	99.8	246282	9	HS091328 Human hered
14	4958.8	99.2	237326	6	BD084122 Polymorph
15	4957.2	99.1	12146	6	AR199263 Sequence
16	4957.2	99.1	12146	6	AR275782 Sequence
17	4957.2	99.1	12146	9	Z92910 Homo sapien
18	4888.8	97.8	11214	9	AF447807 Pan trogl
19	4858.2	97.2	193752	2	AL359892 Homo sapi

20	4607.8	92.2	5982	6	AX701831 Sequence
21	2556.4	51.1	8622	6	AX347044 Sequence
22	2248.8	45.0	8622	6	AX347045 Sequence
23	1071.8	21.4	1865	9	AK123489 Homo sapi
24	832.2	16.6	874	9	Y09800 H.sapiens H
25	740.2	14.8	3334	4	AF301591 Ceratophe
26	657	13.1	761	9	Y09801 H.sapiens H
27	562.2	11.2	4349	4	AF301592 Dicerob b
28	360	7.2	3043	9	AF204869 Homo sapi
29	337.4	6.7	129225	9	AC026765 Homo sapi
30	332.6	6.7	177273	9	AC074194 Homo sapi
31	331.8	6.6	167815	2	AC114888 Pan trogl
32	329	6.6	134970	9	AC002504 Homo sapi
33	325.6	6.5	171978	9	AC026271 Homo sapi
34	324.8	6.5	177540	9	AC006538 Homo sapi
35	323.8	6.5	204505	9	AC089983 Homo sapi
36	323.6	6.5	68280	2	AC068879 Homo sapi
37	323.2	6.5	135173	9	AC008806 Homo sapi
38	323.2	6.5	151367	9	AC025750 Homo sapi
39	322.8	6.5	144000	9	AC007621 Homo sapi
40	322.8	6.5	188344	2	AC131617 Homo sapi
41	322.8	6.5	196954	9	AC022148 Homo sapi
42	322.6	6.5	164766	2	AC018350 Homo sapi
43	322.6	6.5	167127	9	AC097641 Homo sapi
44	322	6.4	99335	9	AC008671 Homo sapi
45	321.6	6.4	112713	9	AL391834 Human DNA

ALIGNMENTS

RESULT 1  
AR117789  
LOCUS AR117789 10825 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 1 from patent US 6140305.  
ACCESSION AR117789  
VERSION AR117789.1 GI:14098695  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10825)  
AUTHORS Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,  
Tsuchihashi,Z. and Wolff,R.K.  
TITLE Hereditary hemochromatosis gene products  
JOURNAL Patent: US 6140305-A 1 31-OCT-2000;  
FEATURES Location/Qualifiers  
source  
1..10825  
/organism="unknown"  
/mol\_type="unassigned DNA"

Parent  
clms to polypeptide:

Query Match	100.0%;	Score 5000;	DB 6;	Length 10825;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 5000;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	TCTAAGGTTGAGATAAAATTTTAAATGTATGATTGAATTTTGAATAATCATATAATTTA	60	
Db	1	TCTAAGGTTGAGATAAAATTTTAAATGTATGATTGAATTTTGAATAATCATATAATTTA	60	
QY	61	AATATCTAAAGTTTCAGATCAGAACATTGCGAAGCTACTTTCCCAATCAACACCCCT	120	
Db	61	AATATCTAAAGTTTCAGATCAGAACATTGCGAAGCTACTTTCCCAATCAACACCCCT	120	
QY	121	TCAGATTAAAAACCAAGGGGACACTGGATCAGCTAGTGTTCACAGAGGATACCTT	180	
Db	121	TCAGATTAAAAACCAAGGGGACACTGGATCAGCTAGTGTTCACAGAGGATACCTT	180	
QY	181	CTGCTGTAGGAGAGAGAGAACTAAAGTCTTGAAGACCTGTGTGCTTTTCCACGAGAGTT	240	
Db	181	CTGCTGTAGGAGAGAGAGAACTAAAGTCTTGAAGACCTGTGTGCTTTTCCACGAGAGTT	240	
QY	241	TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGAGAGCCATCCCCG	300	







QY 2461 AGGTAGTGGAGTGGGCTGGGTGGGAACAGAAAAAGGAGTGACAAAACCATTTGTCTCTGAA 2520  
DB 2461 AGGTAGTGGAGTGGGCTGGGTGGGAACAGAAAAAGGAGTGACAAAACCATTTGTCTCTGAA 2520  
QY 2521 TATATTCTGAAGCAAGTCTCTGAAGCATTTCTATTTGTGTGTGAGAGAAAGAGAAATTTGG 2580  
DB 2521 TATATTCTGAAGCAAGTCTCTGAAGCATTTCTATTTGTGTGTGAGAGAAAGAGAAATTTGG 2580  
QY 2581 CTGGGTGTAGTACTCATGCAAGGAGGAGGCCAAGAGAGACAGATTTCTCTGAGCTCAGGA 2640  
DB 2581 CTGGGTGTAGTACTCATGCAAGGAGGAGGCCAAGAGAGACAGATTTCTCTGAGCTCAGGA 2640  
QY 2641 GTTCAAGACAGGCTGGGCAACACAGAAAAACCCCTTCTCTACAAAAATACAAAAATTA 2700  
DB 2641 GTTCAAGACAGGCTGGGCAACACAGAAAAACCCCTTCTCTACAAAAATACAAAAATTA 2700  
QY 2701 GCTGGGTGTGGTGGCATGCACCTGTGATCTAGTACTCTGGGAGGCTGAGGTGGAGGTA 2760  
DB 2701 GCTGGGTGTGGTGGCATGCACCTGTGATCTAGTACTCTGGGAGGCTGAGGTGGAGGTA 2760  
QY 2761 TTGCTTGAGCCAGGAAAGTTGAGGCTGCAGTGAGCCATGACTGTGCACTGTACTTTCAGC 2820  
DB 2761 TTGCTTGAGCCAGGAAAGTTGAGGCTGCAGTGAGCCATGACTGTGCACTGTACTTTCAGC 2820  
QY 2821 CTAGGTGACAGAACAGAACCTGTCTCCCTGACCCCTGAAAAAGAGAGATTTAAAGT 2880  
DB 2821 CTAGGTGACAGAACAGAACCTGTCTCCCTGACCCCTGAAAAAGAGAGATTTAAAGT 2880  
QY 2881 TGACTTTGTCTTTATTTATTTATTTATTTGCTGAGCAGTGGGTAAATTTGGCAATGCCAT 2940  
DB 2881 TGACTTTGTCTTTATTTATTTATTTATTTGCTGAGCAGTGGGTAAATTTGGCAATGCCAT 2940  
QY 2941 TTCTGAGATGGTGAAGCAGAGGAAAGACAGTTTGGGGTAAATCAAGCATCTGCAATTTG 3000  
DB 2941 TTCTGAGATGGTGAAGCAGAGGAAAGACAGTTTGGGGTAAATCAAGCATCTGCAATTTG 3000  
QY 3001 GGACATGTTAAGTTTGAGATTTCCAGTCAGGCTTCCAAAGTGGTGAGGCCACATAGGCAGTT 3060  
DB 3001 GGACATGTTAAGTTTGAGATTTCCAGTCAGGCTTCCAAAGTGGTGAGGCCACATAGGCAGTT 3060  
QY 3061 CAGTGTAAAGATTCAGGACCAAGGCTGGGCAAGGCTGCTCTGTGTAATCCAGCACT 3120  
DB 3061 CAGTGTAAAGATTCAGGACCAAGGCTGGGCAAGGCTGCTCTGTGTAATCCAGCACT 3120  
QY 3121 TTGGTGGCTGAGGACAGGTAGATCATTTGAGGTGAGGATTTGAGACAGCTTTGGCCAA 3180  
DB 3121 TTGGTGGCTGAGGACAGGTAGATCATTTGAGGTGAGGATTTGAGACAGCTTTGGCCAA 3180  
QY 3181 TGGTGAACCCCATGCTTACTTAAATAACAAAAATTTAGCCTGGTGGTGGCGCACGCT 3240  
DB 3181 TGGTGAACCCCATGCTTACTTAAATAACAAAAATTTAGCCTGGTGGTGGCGCACGCT 3240  
QY 3241 ATAGTCCAGGTTTTCAGGAGGCTTAGGTAGGAGATCCCTTGAACCCAGGAGGTGCAGG 3300  
DB 3241 ATAGTCCAGGTTTTCAGGAGGCTTAGGTAGGAGATCCCTTGAACCCAGGAGGTGCAGG 3300  
QY 3301 TTGCAGTGAGCTGAGATTTGTCACCTGCACTCAGCCTGGGTGATAGGTGAGACTCTGT 3360  
DB 3301 TTGCAGTGAGCTGAGATTTGTCACCTGCACTCAGCCTGGGTGATAGGTGAGACTCTGT 3360  
QY 3361 CTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 3420  
DB 3361 CTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 3420  
QY 3421 TCTAATTTGCCCTGAGCACAACCTCTGAGTTCACTACCATGGCTAGACACACCTTTAAC 3480  
DB 3421 TCTAATTTGCCCTGAGCACAACCTCTGAGTTCACTACCATGGCTAGACACACCTTTAAC 3480  
QY 3481 ATTTTCTAGAAATCCACAGCTTTAGTGGAGTCTGTCTATCATGATTTGGAATAGGAT 3540  
DB 3481 ATTTTCTAGAAATCCACAGCTTTAGTGGAGTCTGTCTATCATGATTTGGAATAGGAT 3540

QY 3541 CTGGGGCAGTGAAGGGGTGGCAGCCACGTGTGGCAGAGAAAGCAACAAGAAAGAGC 3600  
DB 3541 CTGGGGCAGTGAAGGGGTGGCAGCCACGTGTGGCAGAGAAAGCAACAAGAAAGAGC 3600  
QY 3601 ACCCAGGACTGTATATGGAAGAAAGACAGGACTGCACTACCCCTTCAAAAATAGGA 3660  
DB 3601 ACCCAGGACTGTATATGGAAGAAAGACAGGACTGCACTACCCCTTCAAAAATAGGA 3660  
QY 3661 CCAGACACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3720  
DB 3661 CCAGACACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3720  
QY 3721 CTCCTACTACACATGGTTAAGGCTTGTGCTCTGCTCCAGGTTTCACTCTCTGCACTA 3780  
DB 3721 CTCCTACTACACATGGTTAAGGCTTGTGCTCTGCTCCAGGTTTCACTCTCTGCACTA 3780  
QY 3781 CCTCTTCAATGGGTGCTCAGACAGGACCTTGGTCTTCTTCTTCTTCTTCTTCTTCTTCT 3840  
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QY 3841 CGTGGATGACCAAGCTTGTCTGTTCTATGATCATGAGAGTCCCGTGTGGAGCCCGCAAC 3900  
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VERSION AR117790.1 GI:14098696  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10825)  
AUTHORS Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,  
Tsuchihashi,Z. and Wolffe,R.K.  
TITLE Hereditary hemochromatosis gene products  
JOURNAL Patent: US 6140305-A 3 31-OCT-2000;  
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DEFINITION Sequence 1 from patent US 6228594.  
ACCESSION AR149459  
VERSION AR149459.1 GI:15114050  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10825)  
AUTHORS Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D.,  
Tsuchihashi, Z., and Wolff, R.K.  
TITLE Method for determining the presence or absence of a hereditary  
hemochromatosis gene mutation  
JOURNAL Patent: US 6228594-A 1 08-MAY-2001;  
FEATURES Location/Qualifiers  
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RESULT 4

AR149460

LOCUS 10825 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 3 from patent US 6228594.

ACCESSION AR149460

VERSION AR149460.1 GI:15114051

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 10825)

AUTHORS Thomas W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D., Tsuchihashi, Z. and Wolff, R.K.

TITLE Method for determining the presence or absence of a hereditary hemochromatosis gene mutation

JOURNAL Patent: US 6228594-A 3 08-MAY-2001;

FEATURES

Location/Qualifiers

source 1..10825

/organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 5000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	3301	TTGCAGTGCAGCTGAGATTTGTCACACTCCAGCTGGGTGATGAGGTGAGACTCTGT	3360
Db	3301	TTGCAGTGCAGCTGAGATTTGTCACACTCCAGCTGGGTGATGAGGTGAGACTCTGT	3360
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Db	3361	CTCAAACTGAAGGAATTTATTCCTCAGGATTTGGG	3420
Qy	3421	TCTAATTTGGCCTTGAGCAACCACTCTCTGAGTTTCAATCACTGGCTGAGACACACCTTTAAC	3480
Db	3421	TCTAATTTGGCCTTGAGCAACCACTCTCTGAGTTTCAATCACTGGCTGAGACACACCTTTAAC	3480
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Db	3481	ATTTTCTTAGAATCCACCAGCTTTTAGTGGAGTCTGTCTTAATCATGAGTATTTGGAAATAGGAT	3540
Qy	3541	CTGGGGCAGTGAGGGGTTGGCACCACGTGCTGGCAGAGAAAAAGCACACAAGGAAAGAGC	3600
Db	3541	CTGGGGCAGTGAGGGGTTGGCACCACGTGCTGGCAGAGAAAAAGCACACAAGGAAAGAGC	3600
Qy	3601	ACCAGGACTGTCTATATGGAAGAAAGACAGGACTGCAACTCCACCTTCAAAAATGAGGA	3660
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KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 246240)  
AUTHORS Feder J.Nathan., Kronmal, G.Scott., Lauer, P.M., Ruddy, D.A.,  
Thomas W., Teuchihaishi, Z. and Wolff, R.K.  
TITLE Megabase transcript map: novel sequences and antibodies thereto  
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QY	2041	CGGCGTGGGGTGGGAGGGGAGTACCATCTGCATGTAGGATGCTAGCAGTATCTGT	2100	QY	3121	TTGGTGGCTGAGGAGGTAGATCATTTTGAGGTTCAGAGTTTCAGACAAGCTTTGGCCAACT	3180
Db	194344	CGGCGTGGGGTGGGAGGGGAGTACCATCTGCATGTAGGATGCTAGCAGTATCTGT	194403	Db	195424	TTGGTGGCTGAGGAGGTAGATCATTTTGAGGTTCAGAGTTTCAGACAAGCTTTGGCCAACT	195483
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QY	2221	ATAAACAAGTAGTGTGGGAGTAGAGCCCAAGAGTAGTAATGGGCTCAGAGAGGA	2280	QY	3301	TTGCACTGAGCTGAGATTTGCGCACTCCAGCTCCAGCTGGGTGATAGAGTGAAGTCTCT	3360
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QY	2461	AGGTAGTGGAGTGGGCTGGGAAACAGAAAGGAGTGAACAAACCAATTTGCTCCTGAA	2520	QY	3541	CTGGGGCAGTGGGGGTGGCAGCCAGCTGTGGCAGAGAAAGCACAAGGAAAGAGC	3600
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ACCESSION AR036574  
VERSION AR036574.1 GI:5953242  
KEYWORDS SOURCE Unknown.  
ORGANISM Unclasseified.  
REFERENCE 1 (bases 1 to 246240)  
AUTHORS Feder,J.Nathan., Kronmal,G.Scott., Lauer,P.M., Ruddy,D.A.,  
Thomas,W., Teuchihashi,Z. and Wolff,R.K.  
TITLE Megabase transcript map: novel sequences and antibodies thereto  
JOURNAL Patent: US 5872237-A 22 16-FEB-1999;  
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Query Match 100.0%; Score 5000; DB 6; Length 246240;  
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DEFINITION Sequence 5 from patent US 6140305.  
ACCESSION AR117791  
VERSION AR117791.1 GI:14098697  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10825)  
AUTHORS Unclassified.  
Thomas, W. J., Drayna, D. T., Feder, J. N., Gnirke, A., Ruddy, D.,  
Tsuchinashi, Z., and Wolff, R. K.  
TITLE Hereditary hemochromatosis gene products  
JOURNAL Patent: US 6140305-A 5 31-OCT-2000;  
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LOCUS AR117792 10825 bp DNA linear PAT 16-MAY-2001
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ACCESSION AR117792
VERSION AR117792.1 GI:14098698
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10825)
AUTHORS Thomas W.J., Drayna D.T., Feder, J.N., Gnirke, A., Ruddy, D.,
Tsuhishashi, Z. and Wolf, R.K.
TITLE Hereditary hemochromatosis gene products
JOURNAL Patent: US 6140305-A 7 31-OCT-2000;
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Best Local Similarity 100.0%; Pred. No. 0;
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ACCESSION AR149462  
VERSION AR149462.1 GI:15114053  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10825)  
AUTHORS Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,  
Tsuchihashi,Z. and Wolff,R.K.  
TITLE Method for determining the presence or absence of a hereditary  
hemochromatosis gene mutation  
JOURNAL Patent: US 6228594-A 7 08-MAY-2001;  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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DB 181 CTGCTGTAGGAGAGAGAGAACTAAAGTTCTCAAGACCTGTGCTTTTCCACAGGAAGTT 240  
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DB 361 ATGGGCCCGGAGCAGGCGCGCTTCTCTCTGATGCTTTTGCAGACCGCGTCTCTG 420  
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  Feder, J.N., Kronmal, G.S., Lauer, P.M., Ruddy, D.A., Thomas, W.J.,
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QY	481	GAAAAATCGAACTAGCTTTTCTTTGCGCTTGGGAGTTTGCTTAACTTTGGAGGACCTGC	540
DB	53498	GAAAAATCGAACTAGCTTTTCTTTGCGCTTGGGAGTTTGCTTAACTTTGGAGGACCTGC	53439
QY	541	TCACCCCTATCCGAGCGCCCTCTCCCTACTTTCTGCTTCCAGACCCCTGAGGGAGTGC	600
DB	53438	TCACCCCTATCCGAGCGCCCTCTCCCTACTTTCTGCTTCCAGACCCCTGAGGGAGTGC	53379
QY	601	CTACCACTGAACTGACAGTAGGGTCCCTCGCCCCAGAGACCTGCCCCCTCCCCCGCTGT	660
DB	53378	CTACCACTGAACTGACAGTAGGGTCCCTCGCCCCAGAGACCTGCCCCCTCCCCCGCTGT	53319
QY	661	CCCGGCTCTGCGAGTGA	720
DB	53318	CCCGGCTCTGCGAGTGA	53259
QY	721	TAAATAAATCTCGTAGTTCCTCACTGAGCTGAGCTTAAGCTTGGAGCTCTTTGAACTGG	780
DB	53258	TAAATAAATCTCGTAGTTCCTCACTGAGCTGAGCTTAAGCTTGGAGCTCTTTGAACTGG	53199
QY	781	AACTCGGGTTATTTTCCAATGTCACTGTGCAAGTTTTCCTCCAGTCACTCCAAACAGG	840
DB	53198	AACTCGGGTTATTTTCCAATGTCACTGTGCAAGTTTTCCTCCAGTCACTCCAAACAGG	53139
QY	841	AAAGTTCTCCCTGAGTGTTCGCGAAGGCTGAGCAAAACCAACAGCAGGATCCGACCG	900
DB	53138	AAAGTTCTCCCTGAGTGTTCGCGAAGGCTGAGCAAAACCAACAGCAGGATCCGACCG	53079
QY	901	GGTTTCCACTCAGAACGAATGCTTGGCGGTGGGGCGCGAAAGAGTGGGCTTGGGA	960
DB	53078	GGTTTCCACTCAGAACGAATGCTTGGCGGTGGGGCGCGAAAGAGTGGGCTTGGGA	53019
QY	961	TCGTAATCTTCAACCACTTTTGTGTGAGACCTGCGGGTGGAGGTCTCTAGGGT	1020
DB	53018	TCGTAATCTTCAACCACTTTTGTGTGAGACCTGCGGGTGGAGGTCTCTAGGGT	52959
QY	1021	GGGAGGCTCCTGAGAGGCGCTACCTCGGGCCCTTTTCCCACTCTTTGGCAATTTGTTCTTTT	1080

DB	52958	GGGAGGCTCCTGAGAGGCGCTACCTCGGGCCCTTTCCCACTCTTGGCAATTTGTTCTTTT	52899
QY	1081	GCTGGAATAATTAAGTATATGTAGTTTGAAGCTTTGAAGTGAACAAATCTCTTTTCGG	1140
DB	52898	GCTGGAATAATTAAGTATATGTAGTTTGAAGCTTTGAAGTGAACAAATCTCTTTTCGG	52839
QY	1141	CTAGGCTTTTATTTGCAATGTGCTGTAAATTAAGAGGCGCTCTCTACAAAGTACTGA	1200
DB	52838	CTAGGCTTTTATTTGCAATGTGCTGTAAATTAAGAGGCGCTCTCTACAAAGTACTGA	52779
QY	1201	TAATGAACATGTAAAGCAATGCACTCTCTTAAGTTTACATTTCAATCTGATCTTATTTGA	1260
DB	52778	TAATGAACATGTAAAGCAATGCACTCTCTTAAGTTTACATTTCAATCTGATCTTATTTGA	52719
QY	1261	TTTTTCACTAGGCGATAGGAGGTAGGAGCTAAATAACGTTTATTTTACTAGAGTTAACT	1320
DB	52718	TTTTTCACTAGGCGATAGGAGGTAGGAGCTAAATAACGTTTATTTTACTAGAGTTAACT	52659
QY	1321	GGAAATTCAGATTAATAAATCTTTTTCAGGTTTACAAAGAACATAAATAATCTGTTTCTG	1380
DB	52658	GGAAATTCAGATTAATAAATCTTTTTCAGGTTTACAAAGAACATAAATAATCTGTTTCTG	52599
QY	1381	ATGTTATTTTCAAGTACTACAGCTGCTTTCTTAATCTTAAAGTTTGAAGTATTTTGGCTGTAG	1440
DB	52598	ATGTTATTTTCAAGTACTACAGCTGCTTTCTTAATCTTAAAGTTTGAAGTATTTTGGCTGTAG	52539
QY	1441	TCTAGCACAGTGTCTGTGGGTGACACCGCGCGCTTCAGCACAGCATTGAGTTTGGTA	1500
DB	52538	TCTAGCACAGTGTCTGTGGGTGACACCGCGCGCTTCAGCACAGCATTGAGTTTGGTA	52479
QY	1501	CTACGCTGATCCACATTTTACACATGACAAAGATGAGGCGATGCGACGGCTGCTTCTCTG	1560
DB	52478	CTACGCTGATCCACATTTTACACATGACAAAGATGAGGCGATGCGACGGCTGCTTCTCTG	52419
QY	1561	CAAAATTTTCAATGCTTACCTGGGCTTTTGGTGGCAGAGCTCATGTCTCCATTCATAGC	1620
DB	52418	CAAAATTTTCAATGCTTACCTGGGCTTTTGGTGGCAGAGCTCATGTCTCCATTCATAGC	52359
QY	1621	TATGATTTTAAACATCAGCTGCAATAGAGGTTGAATAATAAATAATTTTCAATGTTGACAG	1680
DB	52358	TATGATTTTAAACATCAGCTGCAATAGAGGTTGAATAATAAATAATTTTCAATGTTGACAG	52299
QY	1681	AAATATTTTCAATGCTTAAAGTAAATGAGTCCAGGCAATGTTGTCAGCTGTTCAAGCCC	1740
DB	52298	AAATATTTTCAATGCTTAAAGTAAATGAGTCCAGGCAATGTTGTCAGCTGTTCAAGCCC	52239
QY	1741	CAAGGAGAGAGCAGGGAAACAAAGTCTTTTACCTTTTGAATTTTGCATTTCTAGTGGGAGA	1800
DB	52238	CAAGGAGAGAGCAGGGAAACAAAGTCTTTTACCTTTTGAATTTTGCATTTCTAGTGGGAGA	52179
QY	1801	GATGCAATTAAGCAATGAGCAGAAAGATATACACATCAGGAAATCATGGGTGTTGTA	1860
DB	52178	GATGCAATTAAGCAATGAGCAGAAAGATATACACATCAGGAAATCATGGGTGTTGTA	52119
QY	1861	GAGCAGAGAAAGTCAAGGCAAGTCACTCTGGGGCTGACACTTGGAGCAGACATGAAGA	1920
DB	52118	GAGCAGAGAAAGTCAAGGCAAGTCACTCTGGGGCTGACACTTGGAGCAGACATGAAGA	52059
QY	1921	AATAAGAAATGATTTGACTGGGAGCAGTATTTTCCAGGCAAACTGAGTGGGCTTGGCAAG	1980
DB	52058	AATAAGAAATGATTTGACTGGGAGCAGTATTTTCCAGGCAAACTGAGTGGGCTTGGCAAG	51999
QY	1981	TTGGATTTAAAGACGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG	2040
DB	51998	TTGGATTTAAAGACGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG	51939
QY	2041	CGGCGTGGGGTGGGAAGGGGACTTACCATCTGCACTAGGATGCTAGCAGTATCTCTGT	2100
DB	51938	CGGCGTGGGGTGGGAAGGGGACTTACCATCTGCACTAGGATGCTAGCAGTATCTCTGT	51879
QY	2101	CCTCCCTACTCAGTAGGTGCTAGGAGCAGCTCCCGCAGCTTGTGACAAACCAAAATGCTCT	2160



Db	51878	CCTCCTACTCACTAGGCTAGGAGCACTCCCCAGTCTTGACAAACAAAATGTCCT	51819	Qy	3241	ATAGTCCAGGTTTTTCAGGAGGCTTAGGTAGGAGAAATCCCTTGAAACCCAGGAGGTGCAGG	3300
Qy	2161	AAACTTTGCCATGTCACCTAGTATAGACAACTCTCTGGTTAAGAAAGCTCGGGTTGAAAAA	2220	Db	50739	ATAGTCCAGGTTTTTCAGGAGGCTTAGGTAGGAGAAATCCCTTGAAACCCAGGAGGTGCAGG	50680
Db	51818	AAACTTTGCCATGTCACCTAGTATAGACAACTCTCTGGTTAAGAAAGCTCGGGTTGAAAAA	51759	Qy	3301	TTGCAGTGCAGCTGAGATTGTGCCACTGCCACTCCAGCCTGGGTGATAGAGTGAAGATCTGT	3360
Qy	2221	AATAACAAGTAGTGTCTGGGAGTAGAGGCCAAGAGTAGGTAAATGGGCTCAGAAGAGGA	2280	Db	50679	TTGCAGTGCAGCTGAGATTGTGCCACTGCCACTCCAGCCTGGGTGATAGAGTGAAGATCTGT	50620
Db	51758	AATAACAAGTAGTGTCTGGGAGTAGAGGCCAAGAGTAGGTAAATGGGCTCAGAAGAGGA	51699	Qy	3361	CTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA	3420
Qy	2281	GCACAAAAAAGAGTTGTGCAGGCGCTGTAGGCTGTGGTGTGAAATTTCTAGCCAAAGAGTA	2340	Db	50619	CTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA	50560
Db	51698	GCACAAAAAAGAGTTGTGCAGGCGCTGTAGGCTGTGGTGTGAAATTTCTAGCCAAAGAGTA	51639	Qy	3421	TCTAATTTGCCCTGAGCACAACCTCTCAGTTCACACTACCTAGCTGAGTGCAGTGCAGTTC	3480
Qy	2341	ACAGTATCTGTACAGGCTTTTAAAAAGATTGCTCTGGCTGCTATGTGGAAAGCAAGATG	2400	Db	50559	TCTAATTTGCCCTGAGCACAACCTCTCAGTTCACACTACCTAGCTGAGTGCAGTTCAC	50500
Db	51638	ACAGTATCTGTGTACAGGCTTTTAAAAAGATTGCTCTGGCTGCTATGTGGAAAGCAAGATG	51579	Qy	3481	ATTTTCTAGAAATCCACAGCTTTTAGTGGAGTCTGTCTAATCATGAGTATTTGAAATAGGAT	3540
Qy	2401	AAGGAGCAACAGTAAAGCAGGAGGCCAGCCAGGAGCTGTACACAGTCCAGGCAAG	2460	Db	50499	ATTTTCTAGAAATCCACAGCTTTTAGTGGAGTCTGTCTAATCATGAGTATTTGAAATAGGAT	50440
Db	51578	AAGGAGCAACAGTAAAGCAGGAGGCCAGCCAGGAGCTGTACACAGTCCAGGCAAG	51519	Qy	3541	CTGGGGCAGTGAAGGGGTGGCAGCCAGTGTGGCAGAGAAAGCACAAGGAAAGAGC	3600
Qy	2461	AGGTAGTGGAGTGGGCTGGGTCGGAAACAGAAAAGGAGTGAACAAACCAATTTCTCCTGAA	2520	Db	50439	CTGGGGCAGTGAAGGGGTGGCAGCCAGTGTGGCAGAGAAAGCACAAGGAAAGAGC	50380
Db	51518	AGGTAGTGGAGTGGGCTGGGTCGGAAACAGAAAAGGAGTGAACAAACCAATTTCTCCTGAA	51459	Qy	3601	ACCCAGGACTGTATATGGAAGAAAGACAGGACTGCAACTCACCTTCACAAAATGAGGA	3660
Qy	2521	TATATTTGGAAGAAATGCTGAAGGATTTCTATGTTGTGTGAGAGAAAGAGAAAGATTTGG	2580	Db	50379	ACCCAGGACTGTATATGGAAGAAAGACAGGACTGCAACTCACCTTCACAAAATGAGGA	50320
Db	51458	TATATTTGGAAGAAATGCTGAAGGATTTCTATGTTGTGTGAGAGAAAGAGAAAGATTTGG	51399	Qy	3661	CCAGACAGCTGATGGTATGAGTTGATGAGTGTGTGGAGCTTCAACCTCTCCTCTCCC	3720
Qy	2581	CTGGGTGTAGTAGCTCATGCCAAGGAGGAGGCCAAGGAGAGCAGATTCTGTAGCTCAGGA	2640	Db	50319	CCAGACAGCTGATGGTATGAGTTGATGAGTGTGTGGAGCTTCAACCTCTCCTCTCCC	50260
Db	51398	CTGGGTGTAGTAGCTCATGCCAAGGAGGAGGCCAAGGAGAGCAGATTCTGTAGCTCAGGA	51339	Qy	3721	CTCCTACTACATATGTTAAGCCCTGTGTCTGTCTCAGGTTTCACTCTCTGACATA	3780
Qy	2641	GTTCAAGACAGCCCTGGGCAACACAGCAAAACCCCTTCTTACAAAAATACAAAAATTA	2700	Db	50259	CTCCTACTACATATGTTAAGCCCTGTGTCTGTCTCAGGTTTCACTCTCTGACATA	50200
Db	51338	GTTCAAGACAGCCCTGGGCAACACAGCAAAACCCCTTCTTACAAAAATACAAAAATTA	51279	Qy	3781	CCTCTTCAATGGTGCCTCAGAGCAGGACTTGGTCTTCTTCTTGTGAGCTTTGGGCTTA	3840
Qy	2701	GCTGGGTGTGGGATGCACTGTGATCTAGTACTCTGGAGGCTGAGGTGGAGGTA	2760	Db	50199	CCTCTTCAATGGTGCCTCAGAGCAGGACTTGGTCTTCTTCTTGTGAGCTTTGGGCTTA	50140
Db	51278	GCTGGGTGTGGGATGCACTGTGATCTAGTACTCTGGAGGCTGAGGTGGAGGTA	51219	Qy	3841	CGTGATCAGCAGCTGTTTCGTCTTCTATGATCATGAGAGTGCCTGTGGAGCCCGAAC	3900
Qy	2761	TTGCTTTGAGCCAGGAAGTTGAGGCTGCAGTCAGCCATGACTGTGCCACTGTACTTCAGC	2820	Db	50139	CGTGATCAGCAGCTGTTTCGTCTTCTATGATCATGAGAGTGCCTGTGGAGCCCGAAC	50080
Db	51218	TTGCTTTGAGCCAGGAAGTTGAGGCTGCAGTCAGCCATGACTGTGCCACTGTACTTCAGC	51159	Qy	3901	TCCATGGGTTTCCAGTAGAAATTTCAAGCCAGATGTGGCTGCAAGTGTGAGTCTGAA	3960
Qy	2821	CTAGGTGACAGAGCAAGACCTGTCTCCCTGACCCCTGAAAAAGAGAGATTTAAAGT	2880	Db	50079	TCCATGGGTTTCCAGTAGAAATTTCAAGCCAGATGTGGCTGCAAGTGTGAGTCTGAA	50020
Db	51158	CTAGGTGACAGAGCAAGACCTGTCTCCCTGACCCCTGAAAAAGAGAGATTTAAAGT	51099	Qy	3961	AGGTTGGGATCACATGTTTCACTGTTGACTTCTGGAATATATGGAATATACAAACACAG	4020
Qy	2881	TGACTTTGTTCTTTATTTTAAATTTATTTGGCTGAGCAGTGGGTTAATTTGGCAATGCCAT	2940	Db	50019	AGGTTGGGATCACATGTTTCACTGTTGACTTCTGGAATATATGGAATATACAAACACAG	49960
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Qy	2941	TTCTGAGATGGTGAAGGACAGAAAGACAGTTTGGGTTAATCAAGGATCTGCAATTG	3000	Db	49959	CAAGGTTATGGAGAGGGGCTCACCTTCTCAGAGTTGTGAGAGCTTTTTCATCTTTTC	49900
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Qy	3001	GGACATGTTAAGTTTTCAGATTCCAGTCCAGCTTCCAAGTGGTGGGCCACATAGGCAGTT	3060	Db	49899	ATGCATCTTGAAGGAAAACAGCTGGAAGTCTGAGGTTTGTGGGACGAGGAAAGAGGAAG	49840
Db	50979	GGACATGTTAAGTTTTCAGATTCCAGTCCAGCTTCCAAGTGGTGGGCCACATAGGCAGTT	50920	Qy	4141	GAATTTGCTTCTCAGATCATTTGCTTCTGGGATGTTGGAATATAGGACCTATTTCTTT	4200
Qy	3061	CAGTGTAGAATTCAGGACCAAGGCTGGGCAAGTGGCTCACTTCTGTAATCCAGCACT	3120	Db	49839	GAATTTGCTTCTCAGATCATTTGCTTCTGGGATGTTGGAATATAGGACCTATTTCTTT	49780
Db	50919	CAGTGTAGAATTCAGGACCAAGGCTGGGCAAGTGGCTCACTTCTGTAATCCAGCACT	50860	Qy	4201	TGGTTGAGTTAAACAAAGGCTGGGATTTTTCAGAGTCCCAACCTCTCAGTCTATCTCTG	4260
Qy	3121	TTGTGGCTGAGGCAAGGATGATCATTTGAGGTGAGGTTTTCAGACAAAGCTTTGGCCACA	3180	Db	49779	TGGTTGAGTTAAACAAAGGCTGGGATTTTTCAGAGTCCCAACCTCTCAGTCTATCTCTG	49720
Db	50859	TTGGTGGCTGAGGCAAGGATGATCATTTGAGGTGAGGTTTTCAGACAAAGCTTTGGCCACA	50800	Qy	4261	GGCTGTGAAATGCAAGAAAGACAAAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG	4320
Qy	3181	TGGTGAACCCCATGTCTACTAAAAATACAAAAATTTAGCCTGGTGTGGTGGCGCAGCCT	3240	Db	49719	GGCTGTGAAATGCAAGAAAGACAAAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG	49660
Db	50799	TGGTGAACCCCATGTCTACTAAAAATACAAAAATTTAGCCTGGTGTGGTGGCGCAGCCT	50740				







QY	841	AAGTTCTTCTCTGAGTCTGTCGCCGAGAAGGCTGAGCAAAACCCACAGCAGGATCCGACGG	900
Db	46261	AAGTTCTTCTCTGAGTCTGTCGCCGAGAAGGCTGAGCAAAACCCACAGCAGGATCCGACGG	46202
QY	901	GGTTTCCACCTCAGAAAGCAATGCGTTGGCGCGTGGGGCGCGGAAAGAGTGGCGTTGGGGA	960
Db	46201	GGTTTCCACCTCAGAAAGCAATGCGTTGGCGCGTGGGGCGCGGAAAGAGTGGCGTTGGGGA	46142
QY	961	TCTGAATTTCTTACACATTTCCACCCACATTTTGGTGTGAGACCTGGGGTGGAGGCTCTTAGGCT	1020
Db	46141	TCTGAATTTCTTACACATTTCCACCCACATTTTGGTGTGAGACCTGGGGTGGAGGCTCTTAGGCT	46082
QY	1021	GGGAGGCTCTGAGAGAGGCTACCTCGGCGCTTTCCCACTCTTTGGCAATTTGTTCTTTT	1080
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QY	1081	GCCTGGAAATTAAGTATATATGTTAGTTTGAACGTTTGAACGAACTCTCTTTTCGG	1140
Db	46021	GCCTGGAAATTAAGTATATATGTTAGTTTGAACGTTTGAACGAACTCTCTTTTCGG	45962
QY	1141	CTAGGCTTTATGATTTTGCATTTGCTGTAATTAAGAGGCTCTCTACAAAGTACTGA	1200
Db	45961	CTAGGCTTTATGATTTTGCATTTGCTGTAATTAAGAGGCTCTCTACAAAGTACTGA	45902
QY	1201	TAATGAACATGTAAGCAATGCATCTTCTAAGTTTACATTCATATCTGATCTTATTTGA	1260
Db	45901	TAATGAACATGTAAGCAATGCATCTTCTAAGTTTACATTCATATCTGATCTTATTTGA	45842
QY	1261	TTTTTCACTTAGCATAGGAGGTAGGAGCTTAATAATACGTTTATTTTACTAGAGTTTACT	1320
Db	45841	TTTTTCACTTAGGCAATAGGAGGTAGGAGCTTAATAATACGTTTATTTTACTAGAGTTTACT	45782
QY	1321	GGAATTCAGATTATATAACTCTTTTTCAGGTTTACAAAGAACATAAAATACTGGTTTCTG	1380
Db	45781	GGAATTCAGATTATATAACTCTTTTTCAGGTTTACAAAGAACATAAAATACTGGTTTCTG	45722
QY	1381	ATGTTATTTCAAGTACTACAGCTGCTTCTAACTTTAAGTTTGAAGTATTTTGGCCCTGTAG	1440
Db	45721	ATGTTATTTCAAGTACTACAGCTGCTTCTAACTTTAAGTTTGAAGTATTTTGGCCCTGTAG	45662
QY	1441	TGTAGCACAGTGTCTGTGGGTACACGCGCGCTTCAGCACAGACATTTTGAGTTTGTGA	1500
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Db	45601	CTACGTGTATCCACATTTTACATGACAGAAATAGGCATGGCAGCGCTGCTTCTCTGG	45542
QY	1561	CAAAATTTATTCAAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC	1620
Db	45541	CAAAATTTATTCAAATGGTACACGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC	45482
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Db	45481	TATGATTTCTTAAACATCCACACTGCTATTTAGAGTGTGAATAATAAAATTTTCATGTTCGAGCAG	45422
QY	1681	AAATATTCTATTTGTATCAAGTGTAAATGAGTCCCGCATGTGTGTGCACTGTTCAGGCC	1740
Db	45421	AAATATTCTATTTGTATCAAGTGTAAATGAGTCCCGCATGTGTGTGCACTGTTCAGGCC	45362
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Db	45361	CAAGGGAGAGCAGGGAACAAGTCTTTTACCTTTTGATATTTTGCATCTTAGTGGGAGA	45302
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Db	45301	GATGACAAATAGCAAAATGAGCAGAAAGATATACAACTCAGGAATCATGGGTGTTGTGA	45242
QY	1861	GAAGCAGAGAGTCAGGGCAAGTCACTCTGGGCTGACACTTGTAGCAGAGACATGAAGA	1920
Db	45241	GAAGCAGAGAGTCAGGGCAAGTCACTCTGGGCTGACACTTGTAGCAGAGACATGAAGA	45182

[illegible]







REFERENCE	1 (bases 1 to 12146)	
AUTHORS	Rothenberg,B.E.; Sawada-Hirai,R. and Barton,J.C.	
TITLE	Mutations associated with iron disorders	
JOURNAL	Patent: US 6355425-A 27 12-MAR-2002;	
FEATURES	Location/Qualifiers	
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	/organism="unknown"	
	/mol_type="unassigned DNA"	
ORIGIN		
	Query Match 99.1%; Score 4957.2; DB 6; Length 12146;	
	Best Local Similarity 99.8%; Pred. No. 0;	
	Matches 4995; Conservative 0; Mismatches 3; Indels 6; Gaps 3;	
QY	1 TCTAAGGTTGAGATAAAATTTTAAATGTATGATTTGAATTTTGAATAATCATAAATATTTA 60	
DB	889 TCTAAGGTTGAGATAAAATTTTAAATGTATGATTTGAATTTTGAATAATCATAAATATTTA 948	
QY	61 AATATCTAAAGTTTCAGATCAGAACATTTGGAAGCTACTTTTCCCAATCAACAAACCCCT 120	
DB	949 AATATCTAAAGTTTCAGATCAGAACATTTGGAAGCTACTTTTCCCAATCAACAAACCCCT 1008	
QY	121 TCAGGATTTAAACCAAGGGGGACACTGGATCACCTAGTGTGTTTCAACAGCAGGTACCTT 180	
DB	1009 TCAGGATTTAAACCAAGGGGGACACTGGATCACCTAGTGTGTTTCAACAGCAGGTACCTT 1068	
QY	181 CTGCTGTAGGAGAGAGAGAACTAAAGTTCTGAAAGCTGTGTTGCTTTTCAACAGGAATT 240	
DB	1069 CTGCTGTAGGAGAGAGAGAACTAAAGTTCTGAAAGCTGTGTTGCTTTTCAACAGGAATT 1128	
QY	241 TTACTGGGCATCTCTGAGCTAGGCAATAGCTGTAGGTGACTTCTGGAGCCATCCCG 300	
DB	1129 TTACTGGGCATCTCTGAGCTAGGCAATAGCTGTAGGTGACTTCTGGAGCCATCCCG 1188	
QY	301 TTTCCCGCCCCCAAGAGCGGAGATTTAAACGGGACGTGCGGGCAGAGCTCGGGAA 360	
DB	1189 TTTCCCGCCCCCAAGAGCGGAGATTTAAACGGGACGTGCGGGCAGAGCTCGGGAA 1248	
QY	361 ATGGGCGCGAGACGAGCGCGCTTCTCTCTGTATGCTTTTGAGACCGCGGTCTG 420	
DB	1249 ATGGGCGCGAGACGAGCGCGCTTCTCTCTGTATGCTTTTGAGACCGCGGTCTG 1308	
QY	421 CAGGGCGCTTCTCGTGAGTCCGAGGCTCGCGGCGAACTAGGGCGCGCGGGGTG 480	
DB	1309 CAGGGCGCTTCTCGTGAGTCCGAGGCTCGCGGCGAACTAGGGCGCGCGGGGTG 1368	
QY	481 GAAATCGAACTAGCTTTTCTTTTGGCTTTGGGAGTTTGCTAACTTTGGAGGACCTGC 540	
DB	1369 GAAATCGAACTAGCTTTTCTTTTGGCTTTGGGAGTTTGCTAACTTTGGAGGACCTGC 1428	
QY	541 TCAACCTATCCGGAAGCCCTCTCCCTACTTTTCTGGTTCAGACCCCGTGAGGAGTGC 600	
DB	1429 TCAACCCCAATCCGGAAGCCCTCTCCCTACTTTTCTGGTTCAGACCCCGTGAGGAGTGC 1488	
QY	601 CTACACCTGAATGAGAGTAGGGTCCCTCGCCCCAGGACCTGCCCCCTCCCGGGCTGT 660	
DB	1489 CTACACCTGAATGAGAGTAGGGTCCCTCGCCCCAGGACCTGCCCCCTCCCGGGCTGT 1548	
QY	661 CCGGCTCTGGCGAGTGAATTTTGGAAACCGCCCACTCCCTTCCCCCAACTAGAAATGCTTT 720	
DB	1549 CCGGCTCTGGCGAGTGAATTTTGGAAACCGCCCACTCCCTTCCCCCAACTAGAAATGCTTT 1608	
QY	721 TAAATAATCTCGTAGTTCTCTCACTGAGCTGAGCTTAAGCTTGGGGCTCTTTGAACCTGG 780	
DB	1609 TAAATAATCTCGTAGTTCTCTCACTGAGCTGAGCTTAAGCTTGGGGCTCTTTGAACCTGG 1668	
QY	781 AACTCGGGTTATTTTCCAATGTCAGTGTGCAAGTTTTCGCCAGTCACTCCCAACAGG 840	
DB	1669 AACTCGGGTTATTTTCCAATGTCAGTGTGCAAGTTTTCGCCAGTCACTCCCAACAGG 1728	
QY	841 AAGTTCTTCCCTGAGTGTTCGAGAGGCTGAGCAAAACCAACAGCAGGATCCGACGG 900	
DB	1729 AAGTTCTTCCCTGAGTGTTCGAGAGGCTGAGCAAAACCAACAGCAGGATCCGACGG 1788	

QY	901 GGTTCACCTCAGAACGAATGCGTTGGCGGTGGGGCGCGAAGAGCTGGGTTGGGA 960	
DB	1789 GGTTCACCTCAGAACGAATGCGTTGGCGGTGGGGCGCGAAGAGCTGGGTTGGGA 1848	
QY	961 TCTGAATTTCTTCAACCATTCCACCCACTTTTGGTGAAGCTCGGGGTGAGGCTCTTAGGT 1020	
DB	1849 TCTGAATTTCTTCAACCATTCCACCCACTTTTGGTGAAGCTCGGGGTGAGGCTCTTAGGT 1908	
QY	1021 GGGAGGCTCTGAGAGAGGCTTACCTCGGGCTTTTCCCACTCTTTGGCAATTTGTTCTTTT 1080	
DB	1909 GGGAGGCTCTGAGAGAGGCTTACCTCGGGCTTTTCCCACTCTTTGGCAATTTGTTCTTTT 1968	
QY	1081 GCCTGGAAATTTAGTATATCTTGTAGTTTGAACGTTTGAACCTGAACAAATCTCTTTTCGG 1140	
DB	1969 GCCTGGAAATTTAGTATATCTTGTAGTTTGAACGTTTGAACCTGAACAAATCTCTTTTCGG 2028	
QY	1141 CTAGGCTTTATTTGATTTTCAATGTCTGTAAATTTAAGAGGCTCTCTACAAAGTACTGA 1200	
DB	2029 CTAGGCTTTATTTGATTTTCAATGTCTGTAAATTTAAGAGGCTCTCTACAAAGTACTGA 2088	
QY	1201 TAATGAACATGTAAAGCAATGCACTCATTCTAAAGTTTACATCATATCTGATCTTATTTGA 1260	
DB	2089 TAATGAACATGTAAAGCAATGCACTCATTCTAAAGTTTACATCATATCTGATCTTATTTGA 2148	
QY	1261 TTTTCACTAGGATAGGAGGCTAGGAGCTAATATACGTTTATTTTACTAGAAAGTAACT 1320	
DB	2149 TTTTCACTAGGATAGGAGGCTAGGAGCTAATATACGTTTATTTTACTAGAAAGTAACT 2208	
QY	1321 GGAATTCAGATTTATATAACTCTTTTCAGGTTTACAAAGAACATAATAATCTGGTTTCTG 1380	
DB	2209 GGAATTCAGATTTATATAACTCTTTTCAGGTTTACAAAGAACATAATAATCTGGTTTCTG 2268	
QY	1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTTGAAGTATTTTGCCTCTGAG 1440	
DB	2269 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTTGAAGTATTTTGCCTCTGAG 2328	
QY	1441 TGTAGCAGTGTCTTGTGGGTCAACGCGCGCTCAGCAGCAGCACTTTGAGTTTGGTA 1500	
DB	2329 TGTAGCAGTGTCTTGTGGGTCAACGCGCGCTCAGCAGCAGCACTTTGAGTTTGGTA 2388	
QY	1501 CTACGTGTATCCACATTTTACACATGACAAAGATGAGGATGAGCAAGGCTCTTCTG 1560	
DB	2389 CTACGTGTATCCACATTTTACACATGACAAAGATGAGGATGAGCAAGGCTCTTCTG 2448	
QY	1561 CAAATTTATCAATGGTACACCTGCGGCTTTGGTGGCAGAGCTCATGTCCTCATGAC 1620	
DB	2449 CAAATTTATCAATGGTACACCTGCGGCTTTGGTGGCAGAGCTCATGTCCTCATGAC 2508	
QY	1621 TATGATTTCTTAAACATCACCTGCAATTAGAGTTGAATAATAAAATTTTCATGTTGAGCAG 1680	
DB	2509 TATGATTTCTTAAACATCACCTGCAATTAGAGTTGAATAATAAAATTTTCATGTTGAGCAG 2568	
QY	1681 AAATATTCAATTTTACAAAGTGTAAATGAGTCCCAAGCCTGTTGTCACCTGTTCAAGCCC 1740	
DB	2569 AAATATTCAATTTTACAAAGTGTAAATGAGTCCCAAGCCTGTTGTCACCTGTTCAAGCCC 2628	
QY	1741 CAAGGAGAGAGCAGGGAAAACAAGTCTTTTACCTTTTGTATATTTTGCATTTCTAGTGGGAGA 1800	
DB	2629 CAAGGAGAGAGCAGGGAAAACAAGTCTTTTACCTTTTGTATATTTTGCATTTCTAGTGGGAGA 2688	
QY	1801 GATGCAATTAAGCAATCAGCAGAAAGATATACAAATCAGGAAATCATGGGTGTTTGA 1860	
DB	2689 GATGCAATTAAGCAATCAGCAGAAAGATATACAAATCAGGAAATCATGGGTGTTTGA 2748	
QY	1861 GAAACAGAGAGTTCAGGGCAAGTCACTCTGGGGCTGACACTTTGAGCAGAGACATGAAGA 1920	
DB	2749 GAAACAGAGAGTTCAGGGCAAGTCACTCTGGGGCTGACACTTTGAGCAGAGACATGAAGA 2808	
QY	1921 AATAAGAAATGATATTGACTGGAGCAGTATTTTCCAGGCAAACTCAGTGGGCTGGCAG 1980	
DB	2809 AATAAGAAATGATATTGACTGGAGCAGTATTTTCCAGGCAAACTCAGTGGGCTGGCAG 2868	







Db 5027 GAAGGAATTTGCTTCTGAGATCATTTGGTCTTGGGGATGGTGAATAAGGACCTATT 5086  
QY 4197 CCTTTGGTTGCAGTTTAA CAAGCTGGGATTTTTCCAGAGTCCACACCCCTGCAGGTCA 4256  
Db 5087 CCTTTGGTTGCAGTTTAA CAAGCTGGGATTTTTCCAGAGTCCACACCCCTGCAGGTCA 5146  
QY 4257 CCTGGGCTGTGAAATGCAAGACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGA 4316  
Db 5147 CCTGGGCTGTGAAATGCAAGACAAACAGTACCGAGGGCTACTGGAAGTACGGGTATGA 5206  
QY 4317 TGGGCAGGACCACTTGAATTTCTGCCCTGCACACACTGGATTGGAGAGCAGAGACCCAG 4376  
Db 5207 TGGGCAGGACCACTTGAATTTCTGCCCTGCACACACTGGATTGGAGAGCAGAGACCCAG 5266  
QY 4377 GGCCTGGCCCCAACAAAGCTGGAATGGGAAAGGCACAAAGATTGGGGCCAGGCAGAAACAGGGC 4436  
Db 5267 GGCCTGGCCCCAACAAAGCTGGAATGGGAAAGGCACAAAGATTGGGGCCAGGCAGAAACAGGGC 5326  
QY 4437 CTACCTGGAGAGGAGTGCCTTGCACAGCTGCAGCAGTGTCTGGAGCTGGGGAGAGGTGT 4496  
Db 5327 CTACCTGGAGAGGAGTGCCTTGCACAGCTGCAGCAGTGTCTGGAGCTGGGGAGAGGTGT 5386  
QY 4497 TTTGGACCAACAAAGTATGGTGGAAACACACTTCTGCCCTATATCTCTAGTGGCAGAGTG 4556  
Db 5387 TTTGGACCAACAAAGTATGGTGGAAACACACTTCTGCCCTATATCTCTAGTGGCAGAGTG 5446  
QY 4557 GAGGAGTTGCAGGCAACCGAATCCCTGGTTGGAGTTTTCAGAGTGGCTGAGGCTGTGTG 4616  
Db 5447 GAGGAGTTGCAGGCAACCGAATCCCTGGTTGGAGTTTTCAGAGTGGCTGAGGCTGTGTG 5506  
QY 4617 CCTCTCCAAATTCGGGAAGGACTTCTCAATCCTAGAGTCTCTACCTTATATTGAGA 4676  
Db 5507 CCTCTCCAAATTCGGGAAGGACTTCTCAATCCTAGAGTCTCTACCTTATATTGAGA 5566  
QY 4677 TGTATGACAGCCCAAGTCAATGGTTTAAATTTCTTCTCCATGCATATGGCTCAAAG 4736  
Db 5567 TGTATGACAGCCCAAGTCAATGGTTTAAATTTCTTCTCCATGCATATGGCTCAAAG 5626  
QY 4737 GGAAGTCTATGGCCCTTGTCTTTTATTTAAACCAATATCTTTTGTATATTTATACCTG 4796  
Db 5627 GGAAGTCTATGGCCCTTGTCTTTTATTTAAACCAATATCTTTTGTATATTTATACCTG 5686  
QY 4797 TTAAAAATTCAGAAATGCAAGCCGGCAGCGTGGCTCACCCCTGTAAATCCAGCACTT 4856  
Db 5687 TTAAAAATTCAGAAATGCAAGCCGGCAGCGTGGCTCACCCCTGTAAATCCAGCACTT 5746  
QY 4857 TGGGAGGCCGAGCGGGTGGTCAAGGTCAGGAGTTTGGAGACCAAGCCCTGACCAACATGG 4916  
Db 5747 TGGGAGGCCGAGCGGGTGGTCAAGGTCAGGAGTTTGGAGACCAAGCCCTGACCAACATGG 5806  
QY 4917 TGAACCCGCTCTCTAAAAAATACAAAAATTAGCTGGTCACAGTCAATCGGCACCTGTAGT 4976  
Db 5807 TGAACCCGCTCTCTAAAAAATACAAAAATTAGCTGGTCACAGTCAATCGGCACCTGTAGT 5866  
QY 4977 CCCAGCTAATTGGAGGCTGAGGC 5000  
Db 5867 CCCAGCTAATTGGAGGCTGAGGC 5890



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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 05:14:23 ; Search time 2556.69 Seconds  
(without alignments)  
11576.980 Million cell updates/sec

Title: US-09-497-957-1\_COPY\_1\_5000

Perfect score: 5000  
Sequence: 1 TCTAAGGTTGAGATAAAATT.....GCTAATTGGAGGCTGAGGC 5000

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5000	100.0	10825	5 AAC68426	Aac68426 Human her
2	5000	100.0	10825	5 AAC68425	Aac68425 Human her
3	5000	100.0	10825	10 ADG87260	Adg87260 Hereditar
4	5000	100.0	10825	10 ADG87262	Adg87262 Hereditar
5	4998.4	100.0	10824	10 ADG87266	Adg87266 Hereditar
6	4998.4	100.0	10825	5 AAC68427	Aac68427 Human her
7	4998.4	100.0	10825	5 AAC68428	Aac68428 Human her
8	4998.4	100.0	10825	10 ADG87264	Adg87264 Hereditar
9	4995.2	99.9	10824	10 ADG87338	Adg87338 Hereditar
10	4995.2	99.9	10825	2 AAT96690	Aat96690 Hereditar
11	4988	99.8	235033	2 AAU57926	Aau57926 Hereditar
12	4957.2	99.1	12146	3 AAU96794	Aau96794 Genomic D
13	4938	98.8	237326	2 AAU57903	Aau57903 Hereditar
14	4607.8	92.2	5982	8 ABV93934	Abv93934 Human col
15	2556.4	51.1	8622	6 ABL34142	Ab134142 Human imm
16	2248.8	45.0	8622	6 ABL34143	Ab134143 Human imm
17	998.4	20.0	5749	4 AAL36747	Aal36747 Human mus
18	998.4	20.0	5749	8 ABX59735	Abx59735 cDNA enco
19	998.4	20.0	5749	12 ADJ30485	Adj30485 Human mus
20	500	10.0	500	12 ACH76934	Ach76934 Human gen

21	420.6	8.4	497	9	ACH27480	Ach27480 Human adu
22	321.2	6.4	32148	4	AAL04218	Aal04218 Human rep
23	321	6.4	1317	6	ABK49917	Abk49917 DNA enco
24	321	6.4	1439	10	ADG87268	Adg87268 Hereditar
25	321	6.4	1439	10	ADG87269	Adg87269 Hereditar
26	321	6.4	1440	2	AAT96691	Aat96691 Hereditar
27	321	6.4	1440	5	AAC68430	Aac68430 Human her
28	321	6.4	1440	5	AAC68432	Aac68432 Human her
29	321	6.4	2506	3	AAU96769	Aau96769 cDNA sequ
30	321	6.4	2727	2	AAU23525	Aau23525 Haemochro
31	321	6.4	2727	11	ADP64956	Adp64956 Human hem
32	321	6.4	2727	11	ADP65373	Adp65373 Human hae
33	319.4	6.4	1439	10	ADG87336	Adg87336 Hereditar
34	319.4	6.4	1439	10	ADG87270	Adg87270 Hereditar
35	319.4	6.4	1439	10	ADG87271	Adg87271 Hereditar
36	319.4	6.4	1440	5	AAC68431	Aac68431 Human her
37	319.4	6.4	1440	5	AAC68432	Aac68432 Human her
38	316.8	6.3	143973	11	ACN44142	Acn44142 Human gen
39	316.6	6.3	2285	13	ADQ38608	Adq38608 Human SNP
40	316.6	6.3	2674	13	ADQ38604	Adq38604 Human SNP
41	316.6	6.3	2716	13	ADQ38602	Adq38602 Human SNP
42	312.4	6.2	46765	6	AAU99306	Aau99306 DNA enco
43	312.4	6.2	126990	12	ADP13332	Adp13332 Renal cel
44	312	6.2	80928	12	ADO25290	Ado25290 Human pro
45	308.8	6.2	78539	8	ACA64942	Aca64942 Human FRA

## ALIGNMENTS

RESULT 1  
AAC68426  
ID AAC68426 standard; DNA; 10825 BP.  
XX  
AC AAC68426;  
XX  
DT 21-FEB-2001 (first entry)  
XX  
DE Human hereditary hemochromatosis 24d1 mutation DNA.  
XX  
KW HH; hereditary hemochromatosis; chelation agent;  
KW T-cell differentiation factor; iron overload; ds.  
XX  
OS Homo sapiens.  
XX  
PN US6140305-A.  
XX  
PD 31-OCT-2000.  
XX  
PF 04-APR-1997; 97US-00834497.  
XX  
PR 04-APR-1996; 96US-00630912.  
PR 16-APR-1996; 96US-00632673.  
PR 23-MAY-1996; 96US-00652265.  
(BIRA ) BIO-RAD LAB INC.  
PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;  
PI Feder JN;  
DR WPI; 2001-006341/01.  
XX P-PSDB; AAB36870.  
XX  
PT New hereditary hemochromatosis gene products or polypeptides, useful for  
PT treating hereditary hemochromatosis in a patient, and as a metal  
PT chelation agent alleviating iron overload.  
PS Disclosure; Fig 3; 108pp; English.  
XX  
CC The present invention relates to hereditary hemochromatosis gene  
CC products. These proteins may be used to treat a patient diagnosed as  
CC having human hemochromatosis disease. It is also useful as a metal  
CC chelation agent or as a T-cell differentiation factor, and for















QY 601 CTACCACTGAATGACAGATAGGGTCCCTCGCCCCCAGGACCTGCCCCCTCCCGCGCTGT 660  
 DB 601 CTACCACTGAATGACAGATAGGGTCCCTCGCCCCCAGGACCTGCCCCCTCCCGCGCTGT 660  
 QY 661 CCGGCTCTCGGAGTGACTTTTGGAAACCGCCCACTCCCTTCCCCCACTAGAACTCTTT 720  
 DB 661 CCGGCTCTCGGAGTGACTTTTGGAAACCGCCCACTCCCTTCCCCCACTAGAACTCTTT 720  
 QY 721 TAAATAAATCTCGTAGTCTCTCACTTGAAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 780  
 DB 721 TAAATAAATCTCGTAGTCTCTCACTTGAAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 780  
 QY 781 AACTCGGGTTATTTCCAAATGTCAGCTGTGCAAGTTTTTCCCAAGTCACTCCAAACAGG 840  
 DB 781 AACTCGGGTTATTTCCAAATGTCAGCTGTGCAAGTTTTTCCCAAGTCACTCCAAACAGG 840  
 QY 841 AAGTTCTTCCCTGAGTGCTTGGCGAAGGCTGAGCAAAACCCACAGCAGGATCCGACCG 900  
 DB 841 AAGTTCTTCCCTGAGTGCTTGGCGAAGGCTGAGCAAAACCCACAGCAGGATCCGACCG 900  
 QY 901 GGTTCACACTCAGAAACGAATGCGTTGGCGGTGGGGCGCGAAAGAGTGGGTTGGGA 960  
 DB 901 GGTTCACACTCAGAAACGAATGCGTTGGCGGTGGGGCGCGAAAGAGTGGGTTGGGA 960  
 QY 961 TCTGAATTTCTCAACCAATCCACCACCTTTTGGTGAGACCTGGGGTGGAGGTCTTAGGGT 1020  
 DB 961 TCTGAATTTCTCAACCAATCCACCACCTTTTGGTGAGACCTGGGGTGGAGGTCTTAGGGT 1020  
 QY 1021 GGGAGGCTCTGAGAGAGGCTACCTCGGGCCCTTCCCACTCTTGGGCAATTTGTTCTTTT 1080  
 DB 1021 GGGAGGCTCTGAGAGAGGCTACCTCGGGCCCTTCCCACTCTTGGGCAATTTGTTCTTTT 1080  
 QY 1081 GCTGTGAATAAAGTATATGTAGTTTGAAGTTTGAAGTGAACAAATTTCTTTTGG 1140  
 DB 1081 GCTGTGAATAAAGTATATGTAGTTTGAAGTTTGAAGTGAACAAATTTCTTTTGG 1140  
 QY 1141 CTAGGCTTTATGATTTGCAATGTGCTGTAATTAAGAGGCTCTCTACAAAGTACTGA 1200  
 DB 1141 CTAGGCTTTATGATTTGCAATGTGCTGTAATTAAGAGGCTCTCTACAAAGTACTGA 1200  
 QY 1201 TAATGAACATGAAGCAATGCACTCTTAAGTTTACATTTACATTTCTATTTGA 1260  
 DB 1201 TAATGAACATGAAGCAATGCACTCTTAAGTTTACATTTACATTTCTATTTGA 1260  
 QY 1261 TTTTCTACTAGGCAATAGGAGTGAAGTAAATAGTCTTATTTTACTAGAGTTAACT 1320  
 DB 1261 TTTTCTACTAGGCAATAGGAGTGAAGTAAATAGTCTTATTTTACTAGAGTTAACT 1320  
 QY 1321 GGAATTCAGATTAATACTCTTTTCAAGTTTACAAAGAACATAAATAAATCTGGTTTCTG 1380  
 DB 1321 GGAATTCAGATTAATACTCTTTTCAAGTTTACAAAGAACATAAATAAATCTGGTTTCTG 1380  
 QY 1381 ATGTTATTTCAAGTACTACAGTGTCTTAATCTTAGTTGACAGTATTTGCGCTGTAG 1440  
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 DB 1561 CAAATTTATTTAATGTACACTGGGCTTTGGTGAGAGCTCATGTCTCCACTTCATAGC 1620  
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 DB 1621 TATGATTTCTTAAACATCAGCTGATTTAGAGTTGAATAAATAAATTTTCAATGTTAGCAG 1680  
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DB 1681 AAATATTTATTTGTTTACAAGTGTAAATGAGTCCAGCCATGTGTTGCACTGTTCAAGCCC 1740  
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 DB 1741 CAAGGGAGAGACAGGAAACAAAGTCTTTTACCTTTGATATTTTGCATTTCTAGTGGAGA 1800  
 QY 1801 GATGACAAATGAAGCAATGAGCAGAAAGATATACACATCAGGAAATCATGGGTGTTGTGA 1860  
 DB 1801 GATGACAAATGAAGCAATGAGCAGAAAGATATACACATCAGGAAATCATGGGTGTTGTGA 1860  
 QY 1861 GAAGCAGAGAACTGAGGGCAAGTCTCTGGGGCTGACACTTGGAGCAGACATGAAGGA 1920  
 DB 1861 GAAGCAGAGAACTGAGGGCAAGTCTCTGGGGCTGACACTTGGAGCAGACATGAAGGA 1920  
 QY 1921 AATAGAAATGATATTTGAATGAGCAGGAGATATTTTCCAGGCAAACTGAGTGGGCTGGCAAG 1980  
 DB 1921 AATAGAAATGATATTTGAATGAGCAGGAGATATTTTCCAGGCAAACTGAGTGGGCTGGCAAG 1980  
 QY 1981 TTTGGATTTAAAAACGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040  
 DB 1981 TTTGGATTTAAAAACGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040  
 QY 2041 CGGCGTGGGGTGGGAAGGGGACTACCATCTGCACTAGGATGTCTAGCAGTATCTCTGT 2100  
 DB 2041 CGGCGTGGGGTGGGAAGGGGACTACCATCTGCACTAGGATGTCTAGCAGTATCTCTGT 2100  
 QY 2101 CCTCCCTACTCACTAGGTGCTAGGAGCACTCCCGAGTCTTTCACAACTCAAAATGTCTCT 2160  
 DB 2101 CCTCCCTACTCACTAGGTGCTAGGAGCACTCCCGAGTCTTTCACAACTCAAAATGTCTCT 2160  
 QY 2161 AAATTTTGGCAATGCTACCTAGTAGACAAACTCTCTGGTTAAGAAAGCTCGGGTTGAAAA 2220  
 DB 2161 AAATTTTGGCAATGCTACCTAGTAGACAAACTCTCTGGTTAAGAAAGCTCGGGTTGAAAA 2220  
 QY 2221 AATAAACAAAGTGTCTGGGAGTAGAGCCAAAGAAAGTAGGTAAATGGGCTCAGAGAGGA 2280  
 DB 2221 AATAAACAAAGTGTCTGGGAGTAGAGCCAAAGAAAGTAGGTAAATGGGCTCAGAGAGGA 2280  
 QY 2281 GCCACAAACAAAGTGTGCGAGCGCTGTAGGCTGTGGGTGAAATTTCTAGCCCAAGAGTA 2340  
 DB 2281 GCCACAAACAAAGTGTGCGAGCGCTGTAGGCTGTGGGTGAAATTTCTAGCCCAAGAGTA 2340  
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 DB 2341 ACAGTGTATCTGTACAGGCTTTTAAAAAGTTCTCTGGCTGTATGTGAAAAAGCAAAATG 2400  
 QY 2401 AAGGAGCAACAAAGTAAAGAGGAGCCAGCCAGCAAGCTGTACACAGTCCAGGCAAG 2460  
 DB 2401 AAGGAGCAACAAAGTAAAGAGGAGCCAGCCAGCAAGCTGTACACAGTCCAGGCAAG 2460  
 QY 2461 AGGTAGTGGAGTGGGCTGGGTGGGAACAGAAAGGAGTGACAAACCAATTTGTTCTCTGAA 2520  
 DB 2461 AGGTAGTGGAGTGGGCTGGGTGGGAACAGAAAGGAGTGACAAACCAATTTGTTCTCTGAA 2520  
 QY 2521 TATATTTCTGAAGGAATGTGCTGAAGGATTTCTATTTGTGTGAGAAAGAGAAATTTG 2580  
 DB 2521 TATATTTCTGAAGGAATGTGCTGAAGGATTTCTATTTGTGTGAGAAAGAGAAATTTG 2580  
 QY 2581 CTGGGTGTAGTGTCTCATGCCAAGGAGGAGCCAGAGGAGCAGATTTCTGAGCTCAGGA 2640  
 DB 2581 CTGGGTGTAGTGTCTCATGCCAAGGAGGAGCCAGAGGAGCAGATTTCTGAGCTCAGGA 2640  
 QY 2641 GTTTCAGGACCAAGCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA 2700  
 DB 2641 GTTTCAGGACCAAGCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA 2700  
 QY 2701 GCTGGGTGTGGTGGCATGCACCTGTGATCTAGCTACTCGGAGGCTGAGGTTGGGGTA 2760  
 DB 2701 GCTGGGTGTGGTGGCATGCACCTGTGATCTAGCTACTCGGAGGCTGAGGTTGGGGTA 2760  
 QY 2761 TTGCTTGAAGCCGAGGAAGTTGAGGCTGAGGCTGAGCAGCATGATGTGCTCATCTTCAAGC 2820







QY 4981 GCTAATTGGAAGCTGAGGC 5000  
Db ADG87260  
4981 GCTAATTGGAAGCTGAGGC 5000

RESULT 3

ADG87260  
ID ADG87260 standard; DNA; 10825 BP.

XX AC ADG87260;

XX DT 11-MAR-2004 (first entry)

XX DE Hereditary haemochromatosis (HH) wild-type genomic DNA.

XX KW Hereditary haemochromatosis; HH; inherited disorder; iron metabolism;  
KW cirrhosis; diabetes; illness, gene therapy; hepatotropic; gene;  
XX chromosome 6; ds.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT CDS 361..7147

FT /tag= b

FT /product= "Hereditary haemochromatosis wild-type protein"

FT exon 361..436

FT /tag= a

FT intron 437..3761

FT /tag= c

FT exon 3762..4025

FT /tag= d

FT mutation replace(3872,G)

FT /tag= e

FT mutation /note= "24d2 mutation"

FT replace(3878,T)

FT /tag= f

FT intron /note= "24d7 mutation"

FT 4026..4234

FT /tag= g

FT exon 4235..4510

FT /tag= h

FT intron 4511..5605

FT /tag= i

FT exon 5606..5881

FT /tag= j

FT mutation replace(5834,A)

FT /tag= k

FT intron /note= "24d1 mutation"

FT 5882..6039

FT /tag= l

FT exon 6040..6153

FT /tag= m

FT intron 6154..7106

FT /tag= n

FT exon 7107..7147

FT /tag= o

XX US2003148972-A1.

XX PD 07-AUG-2003.

XX 02-MAY-2002; 2002US-00138888.

XX 04-APR-1996; 96US-00630912.

XX 16-APR-1996; 96US-00632673.

XX 23-MAY-1996; 96US-00652265.

XX 04-APR-1997; 97US-00834497.

XX 04-FEB-2000; 2000US-00497957.

XX (BIRA ) BIO-RAD LAB INC.

XX Thomas WJ, Drayna DT, Feder JN, Gnirke A, Ruddy D, Tauchihashi Z;

PI Wolff RK;

XX WPI; 2003-897595/82.  
DR P-PSDB; ADG87261.  
XX  
PT New hereditary hemochromatosis (HH) nucleic acids and peptides, useful  
PT for treating HH leading to diabetes, cirrhosis, sterility or other  
PT serious illnesses.  
XX  
PS Claim 1; SEQ ID NO 1; 122pp; English.  
XX  
CC The present invention relates to gene and mutations thereto, that are  
CC responsible for the disease hereditary haemochromatosis (HH). Sequences  
CC of the invention are useful for treating hereditary haemochromatosis  
CC which is an inherited disorder or iron metabolism where the body  
CC accumulates excess iron. The excess in iron leads to cirrhosis, diabetes,  
CC and other serious illnesses. The invention is also useful in gene  
CC therapy. The present sequence is hereditary haemochromatosis wild-type  
CC genomic DNA located on chromosome 6.  
XX  
SQ Sequence 10825 BP; 2998 A; 2252 C; 2648 G; 2927 T; 0 U; 0 Other;

Query Match 100.0%; Score 5000; DB 10; Length 10825;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTAAGGTTGAGATAAAATTTTAAATGATGATGAAATTTTCAAAATCATAAATATTTA 60

Db 1 TCTAAGGTTGAGATAAAATTTTAAATGATGATGAAATTTTCAAAATCATAAATATTTA 60

QY 61 AATATCTAAAGTTTCAGATCAGAAACATTTGCGAAGCTACTTTTCCCAATCAACACCCCT 120

Db 61 AATATCTAAAGTTTCAGATCAGAAACATTTGCGAAGCTACTTTTCCCAATCAACACCCCT 120

QY 121 TCAGGATTTAAACCAAGGGGGACACTGGATCAGCTAGTGTTCACAGAGGTACCTT 180

Db 121 TCAGGATTTAAACCAAGGGGGACACTGGATCAGCTAGTGTTCACAGAGGTACCTT 180

QY 181 CTGCTGTAGGAGAGAGAACTTAAAGTTCTGAAAGACCTTGTTCCTTTTCCACGAGGAAGTT 240

Db 181 CTGCTGTAGGAGAGAGAACTTAAAGTTCTGAAAGACCTTGTTCCTTTTCCACGAGGAAGTT 240

QY 241 TTACTGGGCACTCTCTGAGCCTAGGCAATAGCTGTAGGCTGATCTTGTGAGGCATCCCCG 300

Db 241 TTACTGGGCACTCTCTGAGCCTAGGCAATAGCTGTAGGCTGATCTTGTGAGGCATCCCCG 300

QY 301 TTTTCCCGCCCCCAAGAGCGGAGATTTAAACGGGGACGTCGCGCCAGAGCTGGGGAA 360

Db 301 TTTTCCCGCCCCCAAGAGCGGAGATTTAAACGGGGACGTCGCGCCAGAGCTGGGGAA 360

QY 361 ATGGGCGCGCGAGCCGCGCTTCTCTCTGATGCTTTTGCAGACCGCGTCTCTG 420

Db 361 ATGGGCGCGCGAGCCGCGCTTCTCTCTGATGCTTTTGCAGACCGCGTCTCTG 420

QY 421 CAGGGGCGCTTGTCTGGTGAATCCAGGGCTCGGGGCGAACTAGGGGCGCGGGGGTG 480

Db 421 CAGGGGCGCTTGTCTGGTGAATCCAGGGCTCGGGGCGAACTAGGGGCGCGGGGGTG 480

QY 481 GAAATATCGAACTAGCTTTTCTTGGCGTTGGGAGTTTGCTAACTTTGGAGGACCTGC 540

Db 481 GAAATATCGAACTAGCTTTTCTTGGCGTTGGGAGTTTGCTAACTTTGGAGGACCTGC 540

QY 541 TCAACCTTATCCGCAAGCCCTCTCCCTACTTTTCTGCGTCCAGACCCCTGAGGGAGTGC 600

Db 541 TCAACCTTATCCGCAAGCCCTCTCCCTACTTTTCTGCGTCCAGACCCCTGAGGGAGTGC 600

QY 601 CTACCACTGAATCGAGATAGGGGTCCCTCGCCCCAGAGACTTGCCTCCCTCCCGGCTGT 660

Db 601 CTACCACTGAATCGAGATAGGGGTCCCTCGCCCCAGAGACTTGCCTCCCTCCCGGCTGT 660

QY 661 CCGGCTCTGGGAGTGACTTTTGGAAACCGCCCACTCCCTTCCCTCCCACTAGAAATGCTTT 720

Db 661 CCGGCTCTGGGAGTGACTTTTGGAAACCGCCCACTCCCTTCCCTCCCACTAGAAATGCTTT 720







2881 TGACTTGTCTTTATTTTAAATTTTATTTGGCTGAGCAGTGGGGTAAATTTGGCAATGCCAT 2940  
2941 TTCTGAGATGGTGAAGGACAGAGAAAGAGCAGTTTGGGGTAAATCAAGGATCTGCATTTTG 3000  
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3001 GGACATGTTAAAGTTTGAAGTTTCCAGTCAGCTTCCAAAGTTGGTGAGGCCACATAGGCAGTT 3060  
3001 GGACATGTTAAAGTTTGAAGTTTCCAGTCAGCTTCCAAAGTTGGTGAGGCCACATAGGCAGTT 3060  
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3061 CAGTGTAAAGTTTCAAGGACCAAGGCTGGGACGGTGGCTCACTTCTGTAAATCCAGCACT 3120  
3121 TTGGTGGCTGAGGACAGGTAGATCAATTTGAGGTCAGGATTTTGAGACAAGCTTTGGCCAAACA 3180  
3121 TTGGTGGCTGAGGACAGGTAGATCAATTTGAGGTCAGGATTTTGAGACAAGCTTTGGCCAAACA 3180  
3181 TGGTGAACCCCATGCTACTAAAAATAAAAAATTAGCTTGGTGGTGCGCAGCT 3240  
3181 TGGTGAACCCCATGCTACTAAAAATAAAAAATTAGCTTGGTGGTGCGCAGCT 3240  
3241 ATAGTCCCAAGTTTTCAGGAGGCTTAGGTAGGAGAAATCCCTTCAACCCAGGAGGTGCAGG 3300  
3241 ATAGTCCCAAGTTTTCAGGAGGCTTAGGTAGGAGAAATCCCTTCAACCCAGGAGGTGCAGG 3300  
3301 TTGCACTGAGCTGAGATTTGCCACTGCACCTCCAGCTGGGTGATAGAGTGCAGCTCTGT 3360  
3301 TTGCACTGAGCTGAGATTTGCCACTGCACCTCCAGCTGGGTGATAGAGTGCAGCTCTGT 3360  
3361 CTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 3420  
3361 CTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 3420  
3421 TCTAATTTGCCCTGAGCACAACCTCTGAGTTCAACTACCATGGCTAGACACACCTTTAAC 3480  
3421 TCTAATTTGCCCTGAGCACAACCTCTGAGTTCAACTACCATGGCTAGACACACCTTTAAC 3480  
3481 ATTTTCTAGAATCCACAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT 3540  
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3541 CTGGGGGACAGTGAAGGGGTGGCAGCACAAGTGTGGCAGAGAAAGACACAAGGAAAGAGC 3600  
3541 CTGGGGGACAGTGAAGGGGTGGCAGCACAAGTGTGGCAGAGAAAGACACAAGGAAAGAGC 3600  
3601 ACCCAGGACTGCATATGAAGAGAAAGACAGGACTGCACCTCTCAAAAATAGAGA 3660  
3601 ACCCAGGACTGCATATGAAGAGAAAGACAGGACTGCACCTCTCAAAAATAGAGA 3660  
3661 CCAGACACAGCTGATGGTATGATGATGCAGGTGTGGAGCCTCAACATCCTGCTCCC 3720  
3661 CCAGACACAGCTGATGGTATGATGATGCAGGTGTGGAGCCTCAACATCCTGCTCCC 3720  
3721 CTCCTACTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3780  
3721 CTCCTACTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3780  
3781 CCTCTTCATGGGTGCTCAGACAGGACCTTGGTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 3840  
3781 CCTCTTCATGGGTGCTCAGACAGGACCTTGGTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 3840  
3841 CGTGGATGACAGCTGCTGCTGCTTCTATCATCATGAGAGTCCCGTGGAGCCCGGAC 3900  
3841 CGTGGATGACAGCTGCTGCTGCTTCTATCATCATGAGAGTCCCGTGGAGCCCGGAC 3900  
3901 TCCATGGGTTCACAGTAGAATTTCAAGCCAGATGTTGGCTGACAGCTGAGTCAAGTCTGAA 3960  
3901 TCCATGGGTTCACAGTAGAATTTCAAGCCAGATGTTGGCTGACAGCTGAGTCAAGTCTGAA 3960  
3961 AGGGTGGGATCAATGTTCACTGTTGACTTCTGGAATATTTAGGAAATATCAAAACACAG 4020  
3961 AGGGTGGGATCAATGTTCACTGTTGACTTCTGGAATATTTAGGAAATATCAAAACACAG 4020

RESULT 4  
ADG87262  
ID ADG87262 standard; DNA; 10825 BP.

4021 CAAGGTATGTGAGAGGGGGCTCACCTTCTCTAGGTTGTCTAGAGCTTTTTCATCTTTTC 4080  
4021 CAAGGTATGTGAGAGGGGGCTCACCTTCTCTAGGTTGTCTAGAGCTTTTTCATCTTTTC 4080  
4081 ATGCATCTTTGAAGGAAACAGCTGGAGTCTGAGGCTTCTGAGGAGCAGGGAAGGAAAG 4140  
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4141 GAATTTGCTTCTGAGATCAATTTGCTTGGGATGTTGGGAAATAGGAAATAGGAAATAGGAAAT 4200  
4141 GAATTTGCTTCTGAGATCAATTTGCTTGGGATGTTGGGAAATAGGAAATAGGAAATAGGAAAT 4200  
4201 TGGTTCAGTTAAACAGGCTGGGGAATTTTCCAGAGTCCCAACCTTCAGAGTTCATCTCTG 4260  
4201 TGGTTCAGTTAAACAGGCTGGGGAATTTTCCAGAGTCCCAACCTTCAGAGTTCATCTCTG 4260  
4261 GGCTGTGAAATCAAGAGAACAAAGTACCGAGGGCTACTGGAAGTACGGGTATGATGG 4320  
4261 GGCTGTGAAATCAAGAGAACAAAGTACCGAGGGCTACTGGAAGTACGGGTATGATGG 4320  
4321 CAGGACCACTTTGAATTTCTGCCCTGCACACACTTGGATTTGGAGAGCAGACACCCAGGGCC 4380  
4321 CAGGACCACTTTGAATTTCTGCCCTGCACACACTTGGATTTGGAGAGCAGACACCCAGGGCC 4380  
4381 TGGCCCAACCAAGCTGGAGTGGGAAAGGCAACAAGTTTGGGGCCAGGCAAGAGGGGCTTAC 4440  
4381 TGGCCCAACCAAGCTGGAGTGGGAAAGGCAACAAGTTTGGGGCCAGGCAAGAGGGGCTTAC 4440  
4441 CTGGAGAGGACTGCTCCCTGCACAGCTGAGAGTGTCTGGAGCTGGGGAGAGGTGTTTG 4500  
4441 CTGGAGAGGACTGCTCCCTGCACAGCTGAGAGTGTCTGGAGCTGGGGAGAGGTGTTTG 4500  
4501 GACCAACAAGGTATGGTGGAAACACACTTCTGCCCTTACTCTAGTGGCAGAGTGGAGG 4560  
4501 GACCAACAAGGTATGGTGGAAACACACTTCTGCCCTTACTCTAGTGGCAGAGTGGAGG 4560  
4561 AGGTTGCAAGGCAACGGAATCCCTGGTGGAGTTTTCAGAGTGGCTGAGGCTGTGTGCCTC 4620  
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4621 TCCAAATCTTGGAAAGGACTTTCTCAATCTCTAGAGTCTCTACCTTATAATTTGAGATGTA 4680  
4621 TCCAAATCTTGGAAAGGACTTTCTCAATCTCTAGAGTCTCTACCTTATAATTTGAGATGTA 4680  
4681 TGAGACAGCACAAGTCAATGGGTTAAATTTCTTTTCTCCATGCATATGGCTCAAGGGAA 4740  
4681 TGAGACAGCACAAGTCAATGGGTTAAATTTCTTTTCTCCATGCATATGGCTCAAGGGAA 4740  
4741 GTGCTCTATGGCCCTTGTCTTTTATTTAAACCAATATCTTTTCTATATTTATACCTGTTAA 4800  
4741 GTGCTCTATGGCCCTTGTCTTTTATTTAAACCAATATCTTTTCTATATTTATACCTGTTAA 4800  
4801 AAATTCAGAAATGTCAAGCCGGGACCGGTGGCTCACCCCTGTAATCCAGACACTTTGGG 4860  
4801 AAATTCAGAAATGTCAAGCCGGGACCGGTGGCTCACCCCTGTAATCCAGACACTTTGGG 4860  
4861 AGGCCGAGCGGGTGGTCAAGGTCAGAGTTCAGAGCCAGCTTCCAGCAACATGGTGAA 4920  
4861 AGGCCGAGCGGGTGGTCAAGGTCAGAGTTCAGAGCCAGCTTCCAGCAACATGGTGAA 4920  
4921 ACCCGCTCTTAAAAAATAACAAAAATAGTGGTCAAGTCAATGGCAGCTCTGTAGTCCCA 4980  
4921 ACCCGCTCTTAAAAAATAACAAAAATAGTGGTCAAGTCAATGGCAGCTCTGTAGTCCCA 4980  
4981 GCTAATTTGGAAGGCTGAGGC 5000  
4981 GCTAATTTGGAAGGCTGAGGC 5000



XX ADG87262;  
XX 11-MAR-2004 (first entry)  
XX Hereditary haemochromatosis (HH) 24d1 mutant genomic DNA.  
XX Hereditary haemochromatosis; HH; inherited disorder; iron metabolism;  
KW cirrhosis; diabetes; illness; gene therapy; hepatotropic; mutant; gene;  
KW ds.  
XX Unidentified.  
XX  
FH Key Location/Qualifiers  
FT CDS 361..7147  
FT FT /\*tag= b  
FT FT /product= "Hereditary haemochromatosis 24d1 mutant  
FT FT protein "  
FT FT 361..436  
FT FT /\*tag= a  
FT FT 437..3761  
FT FT /\*tag= c  
FT FT 3762..4025  
FT FT /\*tag= d  
FT FT 4026..4234  
FT FT /\*tag= e  
FT FT 4235..4510  
FT FT /\*tag= f  
FT FT 4511..5605  
FT FT /\*tag= g  
FT FT 5606..5881  
FT FT /\*tag= h  
FT FT 5882..6039  
FT FT /\*tag= i  
FT FT 6040..6153  
FT FT /\*tag= j  
FT FT 6154..7106  
FT FT /\*tag= k  
FT FT 7107..7147  
FT FT /\*tag= l  
XX US2003148972-A1.  
XX  
XX 07-AUG-2003.  
XX  
XX 02-MAY-2002; 2002US-00138888.  
XX  
XX 04-APR-1996; 96US-00630912.  
XX 16-APR-1996; 96US-00632673.  
XX 23-MAY-1996; 96US-00652285.  
XX 04-APR-1997; 97US-00834497.  
XX 04-FEB-2000; 2000US-00497957.  
XX (BIRA ) BIO-RAD LAB INC.  
XX  
XX Thomas WJ, Drayna DT, Feder JN, Gnirke A, Ruddy D, Tsuchihashi Z;  
PI Wolff RK;  
XX  
XX WPI; 2003-897595/82.  
XX P-PSDB; ADG87263.  
XX  
XX New hereditary hemochromatosis (HH) nucleic acids and peptides, useful  
FT for treating HH leading to diabetes, cirrhosis, sterility or other  
FT serious illnesses.  
XX  
XX Claim 1; SEQ ID NO 3; 122pp; English.  
XX  
XX The present invention relates to gene and mutations thereto, that are  
CC responsible for the disease hereditary haemochromatosis (HH). Sequences  
CC of the invention are useful for treating hereditary haemochromatosis  
CC which is an inherited disorder or iron metabolism where the body  
CC accumulates excess iron. The excess in iron leads to cirrhosis, diabetes,  
CC and other serious illnesses. The invention is also useful in gene

CC therapy. The present sequence is hereditary haemochromatosis 24d1 mutant  
CC genomic DNA.  
XX  
XX Sequence 10825 BP; 2998 A; 2254 C; 2648 G; 2925 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 5000; DB 10; Length 10825;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCTAAGGTGAGATAAAATTTTAAATGATGATGAAATTTTGAATAATCATAAATATTTA 60  
DB 1 TCTAAGGTGAGATAAAATTTTAAATGATGATGAAATTTTGAATAATCATAAATATTTA 60  
QY 61 AATATCTAAAGTTTCTGAGTTCAGATCAGAACATTGCGAAGCTACTTTCCCAATCAACACCCCT 120  
DB 61 AATATCTAAAGTTTCTGAGTTCAGATCAGAACATTGCGAAGCTACTTTCCCAATCAACACCCCT 120  
QY 121 TCAGGATTTAAAAACCAAGGGGACACTGGATCACTAGTGTCTTTCACAAAGCAGGTACCTT 180  
DB 121 TCAGGATTTAAAAACCAAGGGGACACTGGATCACTAGTGTCTTTCACAAAGCAGGTACCTT 180  
QY 181 CTGCTGTAGGAGAGAGAACTAAAGTTTCTGAAAGACCTGTGCTTTTTCACAGGAAGTT 240  
DB 181 CTGCTGTAGGAGAGAGAACTAAAGTTTCTGAAAGACCTGTGCTTTTTCACAGGAAGTT 240  
QY 241 TTACTGGGCATCTCTGAGCCTTAGCANTAGCTGTAGGTTGACTTCTGGAGCCATCCCG 300  
DB 241 TTACTGGGCATCTCTGAGCCTTAGCANTAGCTGTAGGTTGACTTCTGGAGCCATCCCG 300  
QY 301 TTTCCCGCCGCCCAAGAGCGAGATTAAACGGGACCTGGCGGCAGAGCTGGGAA 360  
DB 301 TTTCCCGCCGCCCAAGAGCGAGATTAAACGGGACCTGGCGGCAGAGCTGGGAA 360  
QY 361 ATGGGCCCGGAGCCAGCCGCGCTTCTCTCTGATGCTTTTTCAGACCCGCGTCTG 420  
DB 361 ATGGGCCCGGAGCCAGCCGCGCTTCTCTCTGATGCTTTTTCAGACCCGCGTCTG 420  
QY 421 CAGGGGCGCTTGTGCTGAGTCCGAGGGTCCGCGGCAACTAGGGGCGCGCGGGTG 480  
DB 421 CAGGGGCGCTTGTGCTGAGTCCGAGGGTCCGCGGCAACTAGGGGCGCGCGGGTG 480  
QY 481 GAAAAATCGAAATAGCTTTTCTTGGCTTGGAGTTGCTAACTTTGGAGACCTGC 540  
DB 481 GAAAAATCGAAATAGCTTTTCTTGGCTTGGAGTTGCTAACTTTGGAGACCTGC 540  
QY 541 TCAACCTTATCCGCAAGCCCTCTCCCTACTTTTCTGCTCCAGACCCCGTGAGGAGTGC 600  
DB 541 TCAACCTTATCCGCAAGCCCTCTCCCTACTTTTCTGCTCCAGACCCCGTGAGGAGTGC 600  
QY 601 CTACCACTGAATCGAGATAGGGTCCCTCGCCCGCAGACCTGCCCTCCCGGCTGT 660  
DB 601 CTACCACTGAATCGAGATAGGGTCCCTCGCCCGCAGACCTGCCCTCCCGGCTGT 660  
QY 661 CCCGCTCTGCGAGTGAATTTTGGAAACCGCCACTCCCTTTCCCAACTAGAAATGCTTT 720  
DB 661 CCCGCTCTGCGAGTGAATTTTGGAAACCGCCACTCCCTTTCCCAACTAGAAATGCTTT 720  
QY 721 TAAATAAATCTCGTAGTTCTCTCACTTGAGCTGAGCTAAGCCTTGGGGTCTCTTGAACCTGG 780  
DB 721 TAAATAAATCTCGTAGTTCTCTCACTTGAGCTGAGCTAAGCCTTGGGGTCTCTTGAACCTGG 780  
QY 781 AACTCGGGTTTATTTCCAAATGTCAGTGTGAGTTTTCCTCCAGTCACTCCAAACAGG 840  
DB 781 AACTCGGGTTTATTTCCAAATGTCAGTGTGAGTTTTCCTCCAGTCACTCCAAACAGG 840  
QY 841 AAGTTTCTTCCCTGAGTGTCTTCCGAGAGGCTGAGCAACCCACAGCAGGATCCGACGG 900  
DB 841 AAGTTTCTTCCCTGAGTGTCTTCCGAGAGGCTGAGCAACCCACAGCAGGATCCGACGG 900  
QY 901 GGTTTCCACCTCAGAAACGAAATCGGTGGGGCGGGTGGGGCGGAAAGAGTGGGTTGGGA 960  
DB 901 GGTTTCCACCTCAGAAACGAAATCGGTGGGGCGGGTGGGGCGGAAAGAGTGGGTTGGGA 960



QY 961 TCTGAATTCCTTACCACTTCCACCACTTTTGGTGAGACCTGGGGTGGAGGTCTCTAGGGT 1020  
DB 961 TCTGAATTCCTTACCACTTCCACCACTTTTGGTGAGACCTGGGGTGGAGGTCTCTAGGGT 1020  
QY 1021 GGGAGGCTCTGAGAGAGGCTACCTCGGCCCTTCCCACTCTCGGCAATGTTCTTTT 1080  
DB 1021 GGGAGGCTCTGAGAGAGGCTACCTCGGCCCTTCCCACTCTCGGCAATGTTCTTTT 1080  
QY 1081 GCCTGAAATTAAGTATATGTTAGTTTGAACGTTTGAACCTGAACAAATTCCTTTTCGG 1140  
DB 1081 GCCTGAAATTAAGTATATGTTAGTTTGAACGTTTGAACCTGAACAAATTCCTTTTCGG 1140  
QY 1141 CTAGGCTTTTATGATTTGCAATGCTGTGTAATTAAGAGGCTCTCTCAAAAGTACTGA 1200  
DB 1141 CTAGGCTTTTATGATTTGCAATGCTGTGTAATTAAGAGGCTCTCTCAAAAGTACTGA 1200  
QY 1201 TAATGAACATGTAAGCAATGCACTCACTCTTAAGTTTACATTCATATCTGATCTTATTTGA 1260  
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DB 1321 GGAATTCAGATTAATACTCTTTTCAAGTTTACAAAGAACATAAATACTGTTTCTG 1380  
QY 1381 ATGTTATTTCAAGTACTAGCTGCTTCTAACTTGTAGTTGACAGTATTTTCCCTGTAG 1440  
DB 1381 ATGTTATTTCAAGTACTAGCTGCTTCTAACTTGTAGTTGACAGTATTTTCCCTGTAG 1440  
QY 1441 TGTAGCAGAGTGTCTGTGGGTACACGCGGCTCAGCACAGCAGCTTTGAGTTTGGTA 1500  
DB 1441 TGTAGCAGAGTGTCTGTGGGTACACGCGGCTCAGCACAGCAGCTTTGAGTTTGGTA 1500  
QY 1501 CTACGTTATTCACATTTTACATGACAAAGAAATAGGCAATGGCAGGCTGCTTCTGG 1560  
DB 1501 CTACGTTATTCACATTTTACATGACAAAGAAATAGGCAATGGCAGGCTGCTTCTGG 1560  
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DB 1561 CAAATTTATTCAGTACTAGCTGCTTTGGTGAGAGCTCATGCTCCATCTCATAGC 1620  
QY 1621 TATGATTTCTTAAACATCACATGCAATTAGAGTTGAATAATAAATTTTCAATGAGCAG 1680  
DB 1621 TATGATTTCTTAAACATCACATGCAATTAGAGTTGAATAATAAATTTTCAATGAGCAG 1680  
QY 1681 AAATATTCATTTTCAAGTGTAAATGATCCCAGCCATGTTTGCATGTTCAAGCCC 1740  
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QY 1741 CAAGGAGAGAGCAGGGAACAGTCTTTACCTTTGATATTTTGCATCTAGTGGGAGA 1800  
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QY 1801 GATGACAAATAGCAATGAGCAGAAAGATATACATCAGGAAATCATGGGTGTTTGA 1860  
DB 1801 GATGACAAATAGCAATGAGCAGAAAGATATACATCAGGAAATCATGGGTGTTTGA 1860  
QY 1861 GAAGCAGAGAGTCAAGGCAAGTCTCTGGGGCTGACATTTGAGCAGACATGAAGGA 1920  
DB 1861 GAAGCAGAGAGTCAAGGCAAGTCTCTGGGGCTGACATTTGAGCAGACATGAAGGA 1920  
QY 1921 AATAGAAATGATTTGACTGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAG 1980  
DB 1921 AATAGAAATGATTTGACTGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAG 1980  
QY 1981 TTGGATTTAAAGCGGGTTTCTCAGCACTACTCATGCTGTGTGTGGGGGGGGGG 2040  
DB 1981 TTGGATTTAAAGCGGGTTTCTCAGCACTACTCATGCTGTGTGTGGGGGGGGGGGG 2040  
QY 2041 CGGCGTGGGGTGGGAAGGGGAGCTACCATCTGCATGTAGGATGTCTAGCAGTATCTGT 2100

DB 2041 CGGCGTGGGGTGGGAAGGGGAGCTACCATCTGCATGTAGGATGTCTAGCAGTATCTGT 2100  
QY 2101 CTTCCCTACTCACTAGGTCTAGGAGCACTCCCCAGTCTTGACACCAAAAATGTTCTCT 2160  
DB 2101 CTTCCCTACTCACTAGGTCTAGGAGCACTCCCCAGTCTTGACACCAAAAATGTTCTCT 2160  
QY 2161 AAATTTTGCACATGTCACTAGTAGACAAATCTCTGGTTTAAAGAGCTCGGGTTGAAAA 2220  
DB 2161 AAATTTTGCACATGTCACTAGTAGACAAATCTCTGGTTTAAAGAGCTCGGGTTGAAAA 2220  
QY 2221 AATAAACAAGTATGCTGGGAGTAGAGCCCAAGAAAGTAGGTAATGGGCTCAGAGAGGA 2280  
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QY 2281 GCCACAAAACAAGTGTGCGAGGCTGTAGGCTGTGGTGTGAAATCTAGCCAAAGAGTA 2340  
DB 2281 GCCACAAAACAAGTGTGCGAGGCTGTAGGCTGTGGTGTGAAATCTAGCCAAAGAGTA 2340  
QY 2341 ACAGTGATCTGTACAGGCTTTTAAAGATTTCTCTGGCTGTCTATGTGAAAAGCAGAAATG 2400  
DB 2341 ACAGTGATCTGTACAGGCTTTTAAAGATTTCTCTGGCTGTCTATGTGAAAAGCAGAAATG 2400  
QY 2401 AAGGAGCAACAGTAAAGCAGGAGCCAGCCAGAGAGCTGTTACACAGTCCAGGCAAG 2460  
DB 2401 AAGGAGCAACAGTAAAGCAGGAGCCAGCCAGAGAGCTGTTACACAGTCCAGGCAAG 2460  
QY 2461 AGGTAGTGGAGTGGGCTGGGACAGAAAAGGAGTGAACAAACCATTTCTCTGAA 2520  
DB 2461 AGGTAGTGGAGTGGGCTGGGACAGAAAAGGAGTGAACAAACCATTTCTCTGAA 2520  
QY 2521 TATATTTGAAAGAAATTTGCTGAAGATTTCTATGTTGTGAGAGAAAGAGAAATTTG 2580  
DB 2521 TATATTTGAAAGAAATTTGCTGAAGATTTCTATGTTGTGAGAGAAAGAGAAATTTG 2580  
QY 2581 CTGGGTGTAGTCTCATGCCAAGGAGGAGCCAGAGGAGCAGATTTCTGAGCTCAGGA 2640  
DB 2581 CTGGGTGTAGTCTCATGCCAAGGAGGAGCCAGAGGAGCAGATTTCTGAGCTCAGGA 2640  
QY 2641 GTTCAAGACCAAGCTGGGCAACACAGCAAAACCCCTCTCTACAAAATAACAAAATTA 2700  
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QY 2701 GCTGGTGTGGTGAGTGCACCTGTGATCTCTAGCTCTCGGAGGCTGAGGTGGAGGTA 2760  
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QY 2761 TTGCTTGAGCCAGGAAGTTGAGGCTGAGGAGCAGTGTGCCACTGTACTTTCAGC 2820  
DB 2761 TTGCTTGAGCCAGGAAGTTGAGGCTGAGGAGCAGTGTGCCACTGTACTTTCAGC 2820  
QY 2821 CTAGTGACAGAGCAAGCCCTGTCTCCCTGACCCCTGAAAAGAGAGAGTAAAGT 2880  
DB 2821 CTAGTGACAGAGCAAGCCCTGTCTCCCTGACCCCTGAAAAGAGAGAGTAAAGT 2880  
QY 2881 TGACTTTGTTCTTTATTTTAAATTTTATTTGGCTGAGCAGTGGGTAAATGGCAATGCCAT 2940  
DB 2881 TGACTTTGTTCTTTATTTTAAATTTTATTTGGCTGAGCAGTGGGTAAATGGCAATGCCAT 2940  
QY 2941 TTCTGAGATGTTGAAGGAGGAGGAGTGGGTAAATCAAGGATCTGCATTTG 3000  
DB 2941 TTCTGAGATGTTGAAGGAGGAGGAGTGGGTAAATCAAGGATCTGCATTTG 3000  
QY 3001 GGACATGTTAAGTTTGAGATTTCCAGTCCAGGCTTCCAGTGGTGAGGCCACATAGGAGTT 3060  
DB 3001 GGACATGTTAAGTTTGAGATTTCCAGTCCAGGCTTCCAGTGGTGAGGCCACATAGGAGTT 3060  
QY 3061 CAGTGAAGAATTCAGGACCAAGCTGGGCGAGGCTCACTCTGTAAATCCCAGCACT 3120  
DB 3061 CAGTGAAGAATTCAGGACCAAGCTGGGCGAGGCTCACTCTGTAAATCCCAGCACT 3120  
QY 3121 TTGGTGGCTGAGGAGGAGTATGATTTTCAAGTTCAGGAGTTTGAACAAGCTTGGCCACA 3180  
DB 3121 TTGGTGGCTGAGGAGGAGTATGATTTTCAAGTTCAGGAGTTTGAACAAGCTTGGCCACA 3180



Db	3121	TTGGTGGCTGAGCGCAGGTAGATCAATTTGAGGTGAGGAGTTTGAGACAAGCTTTGGCCACA	3181
Qy	3181	TGGTGAACCCCATCTGTCTACTAAAAATACAAAAATTAGCCTGGTGTGGTGGCGCACGCCT	3240
Db	3181	TGGTGAACCCCATCTGTCTACTAAAAATACAAAAATTAGCCTGGTGTGGTGGCGCACGCCT	3240
Qy	3241	ATAGTCCCAGGTTTTTCAGGAGCGCTTAGGTAGGAGAAATCCCTTTGAACCCAGGAGGTGCAGG	3300
Db	3241	ATAGTCCCAGGTTTTTCAGGAGCGCTTAGGTAGGAGAAATCCCTTTGAACCCAGGAGGTGCAGG	3300
Qy	3301	TTGCAGTCAGCTGAGATTGTGCCACTGCACCTCCAGCCTGGGTGATAGAGTGAGACTCTGT	3360
Db	3301	TTGCAGTCAGCTGAGATTGTGCCACTGCACCTCCAGCCTGGGTGATAGAGTGAGACTCTGT	3360
Qy	3361	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAAGTGAAGGAATATTCTCAGGATTTGGG	3420
Db	3361	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAAGTGAAGGAATATTCTCAGGATTTGGG	3420
Qy	3421	TCTAATTTGGCCTGAGCACCAACTCCTGAGTTCAACTACCATGCTGAGACACACCTTTAAC	3480
Db	3421	TCTAATTTGGCCTGAGCACCAACTCCTGAGTTCAACTACCATGCTGAGACACACCTTTAAC	3480
Qy	3481	ATTTTCTAGATCCACAGCTTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAAATAGAT	3540
Db	3481	ATTTTCTAGATCCACAGCTTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAAATAGAT	3540
Qy	3541	CTGGGGCAGTGAGGGGTGCACGCTGTGTCAGAGAAAAGCACACAAGGAAGAGC	3600
Db	3541	CTGGGGCAGTGAGGGGTGCACGCTGTGTCAGAGAAAAGCACACAAGGAAGAGC	3600
Qy	3601	ACCCAGGACTGTATATGGAAAGAGACAGGACTGCAACTCACCCTTTCAAAAATGAGGA	3660
Db	3601	ACCCAGGACTGTATATGGAAAGAGAGACAGGACTGCAACTCACCCTTTCAAAAATGAGGA	3660
Qy	3661	CCAGACACAGCTGATGTTGATGAGTTGATGAGGTGTGTGGAGCCTCAACATCTGCTCCC	3720
Db	3661	CCAGACACAGCTGATGTTGATGAGTTGATGAGGTGTGTGGAGCCTCAACATCTGCTCCC	3720
Qy	3721	CTCCTACTACATGTTTAAAGGCTGTGCTCTGCTCCAGGTTCAACATCTGCTGCACTA	3780
Db	3721	CTCCTACTACATGTTTAAAGGCTGTGCTCTGCTCCAGGTTCAACATCTGCTGCACTA	3780
Qy	3781	CCTCTTCATGGGTGCCCTCAGACGAGGACCTTGGTCTTTTCTTGTGTAAGCTTTGGGCTA	3840
Db	3781	CCTCTTCATGGGTGCCCTCAGACGAGGACCTTGGTCTTTTCTTGTGTAAGCTTTGGGCTA	3840
Qy	3841	CGTGGATGACAGCTGTTTCTGTTCTATGATCATGAGAGTCGCGGTGAGAGCCCGAAC	3900
Db	3841	CGTGGATGACAGCTGTTTCTGTTCTATGATCATGAGAGTCGCGGTGAGAGCCCGAAC	3900
Qy	3901	TCCATGGTTTTCCAGTAGAATTTCAAGCAGATGTGGCTCAGCTGAGTCAGAGTCTGAA	3960
Db	3901	TCCATGGTTTTCCAGTAGAATTTCAAGCAGATGTGGCTCAGCTGAGTCAGAGTCTGAA	3960
Qy	3961	AGGTTGGGATCACATGTTTCACTGTTGACTTCTTGACTATTATGGAATAATCACAAACACAG	4020
Db	3961	AGGTTGGGATCACATGTTTCACTGTTGACTTCTTGACTATTATGGAATAATCACAAACACAG	4020
Qy	4021	CAAGGGTATGTGGAGAGGGGGCCCTCACCTTCTCAGGTTGTGAGAGTCTTTTCTTTTC	4080
Db	4021	CAAGGGTATGTGGAGAGGGGGCCCTCACCTTCTCAGGTTGTGAGAGTCTTTTCTTTTC	4080
Qy	4081	ATGCATCTTGAAGAAAACAGCTGGAATCTGAGTCTTTGGGAGCAGGGAAGGGAAG	4140
Db	4081	ATGCATCTTGAAGAAAACAGCTGGAATCTGAGTCTTTGGGAGCAGGGAAGGGAAG	4140
Qy	4141	GAAATTTGCTTCTCAGATCATTTTGGTCTTGGGGATGTTGGAAATAGGACCTATTCTTCT	4200
Db	4141	GAAATTTGCTTCTCAGATCATTTTGGTCTTGGGGATGTTGGAAATAGGACCTATTCTTCT	4200
Qy	4201	TGGTTGAGTTAAACAAGCTGGGATTTTTCAGAGTCCACACCTTCGAGGTCACTCTG	4260
Db	4201	TGGTTGAGTTAAACAAGCTGGGATTTTTCAGAGTCCACACCTTCGAGGTCACTCTG	4260

QY	4261	GGCTGTGAAATGCAAGAAGACAACAGTACCAGAGGGCTACTGGAAGTACGGGTATGATGGG	4320
DB	4261	GGCTGTGAAATGCAAGAAGACAACAGTACCAGAGGGCTACTGGAAGTACGGGTATGATGGG	4320
QY	4321	CAGGACCACCTTGAATTTCTGCCCTGCACACTCGATTTGGAGAGCAGCAGAAACCCAGGGCC	4380
DB	4321	CAGGACCACCTTGAATTTCTGCCCTGCACACTCGATTTGGAGAGCAGCAGAAACCCAGGGCC	4380
QY	4381	TGGCCCCACCAAGCTTGGAGTGGGAAGGCACAAGATTCTGGGCTCAGGCAGAAACAGGGCCCTAC	4440
DB	4381	TGGCCCCACCAAGCTTGGAGTGGGAAGGCACAAGATTCTGGGCTCAGGCAGAAACAGGGCCCTAC	4440
QY	4441	CTGAGAGAGGACCTGCCCTGTGCACAGCTGCACAGTTCGACAGTTCGAGCTGGGGAGAGGTGTTTTG	4500
DB	4441	CTGAGAGAGGACCTGCCCTGTGCACAGCTGCACAGTTCGACAGTTCGAGCTGGGGAGAGGTGTTTTG	4500
QY	4501	GACCACAAGGTATGGTGGAAAAACACTTCTGCCCTTATACTCTAGTGGCAGAGTGGAGG	4560
DB	4501	GACCACAAGGTATGGTGGAAAAACACTTCTGCCCTTATACTCTAGTGGCAGAGTGGAGG	4560
QY	4561	AGGTTGCAGGGCACGGAAATCCCTGGTTGGAGTTTTCAGAGGTGGCTGAGGCTGTGTGCCTC	4620
DB	4561	AGGTTGCAGGGCACGGAAATCCCTGGTTGGAGTTTTCAGAGGTGGCTGAGGCTGTGTGCCTC	4620
QY	4621	TCCAAATTCGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACTTATTAATTCAGAGTGTGA	4680
DB	4621	TCCAAATTCGGGAAGGGACTTTCTCAATCCTAGAGTCTCTACTTATTAATTCAGAGTGTGA	4680
QY	4681	TGAGACAGCCACAAGTCATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAGGGAA	4740
DB	4681	TGAGACAGCCACAAGTCATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAGGGAA	4740
QY	4741	GTGTCTATGCCCTTGTCTTTTATTTTAAACCAATAATCTTTTGTATATTTATACCTGTAA	4800
DB	4741	GTGTCTATGCCCTTGTCTTTTATTTTAAACCAATAATCTTTTGTATATTTATACCTGTAA	4800
QY	4801	AAATTCAGAAATGTCAAGGCGGGCAGCGTGGCTCACCCCTGTAAATCCCAAGCACTTTGGG	4860
DB	4801	AAATTCAGAAATGTCAAGGCGGGCAGCGTGGCTCACCCCTGTAAATCCCAAGCACTTTGGG	4860
QY	4861	AGGCCGAGGCGGGTGGTCAAGGTCAAGGTCAGGAGTTTGAGACCAGCCTGCACCAACATGTGAA	4920
DB	4861	AGGCCGAGGCGGGTGGTCAAGGTCAAGGTCAGGAGTTTGAGACCAGCCTGCACCAACATGTGAA	4920
QY	4921	ACCGCTCTCTAAAAAATACAAAAATAGCTGGTGCAGTCACTGCGCACCTGTAGTCCCA	4980
DB	4921	ACCGCTCTCTAAAAAATACAAAAATAGCTGGTGCAGTCACTGCGCACCTGTAGTCCCA	4980
QY	4981	GCTAATTTGGAAGGCTGAGGC	5000
DB	4981	GCTAATTTGGAAGGCTGAGGC	5000

RESULT 5  
ADG87266

ADG87266  
ID ADG87266 standard: DNA: 10824 BP.

AC ADG87266;

11-MAR-2004 (first entry)

DE Hereditary haemochromatosis (HH) mutant genomic DNA.

Hereditary haemochromatosis; HH; inherited disorder; iron metabolism;  
 KW cirrhosis; diabetes; gene therapy; hepatotropic; mutant; gene  
 KW ds.

OS Unidentified.

Key	Location/Qualifiers
CDS	361. .7147
FT	/*tag= b







Db 1201 TAAATGAACATGTAAGCAATGCACTCACCTTCAAGTTACATTCATATCTGATCTTATTTGA 1260  
Qy TTTTTCACATAGGCAATAGGAGGTAGAGCTAATAATACGTTTATTTTACTAGAAAGTTAACT 1320  
Db TTTTTCACATAGGCAATAGGAGGTAGAGCTAATAATACGTTTATTTTACTAGAAAGTTAACT 1320  
Qy GGAAATTCAGATTATATACTCTTTTTCAGGTTACAAGAACACATAAATAATCTGGTTTCTG 1380  
Db GGAAATTCAGATTATATACTCTTTTTCAGGTTACAAGAACACATAAATAATCTGGTTTCTG 1380  
Qy ATGTTATTTTCAAGTACTACAGCTGCTCTTAATCTTTAGTTGACAGTGAATTTTGGCCCTGTAG 1440  
Db ATGTTATTTTCAAGTACTACAGCTGCTCTTAATCTTTAGTTGACAGTGAATTTTGGCCCTGTAG 1440  
Qy TGTAGCAGAGTTCTTGTGGGTCAACGCCGCCCTTCAGCACAGCACTTTGAGTTTGGTA 1500  
Db TGTAGCAGAGTTCTTGTGGGTCAACGCCGCCCTTCAGCACAGCACTTTGAGTTTGGTA 1500  
Qy CTACGCTATCCACATTTTACACATGACAAGAAATGAGGCATGGCACGGCTGCTTCTCTGG 1560  
Db CTACGCTATCCACATTTTACACATGACAAGAAATGAGGCATGGCACGGCTGCTTCTCTGG 1560  
Qy CAAATTTTATTCATGGTACATCTGGGCTTTGGTGCGAGAGCTCATGTCTCCAATTCATAGC 1620  
Db CAAATTTTATTCATGGTACATCTGGGCTTTGGTGCGAGAGCTCATGTCTCCAATTCATAGC 1620  
Qy TATGATTTCTTAAACATCACTGCAATAGAGGTTGAATTAATAAATTTTCAATGTTGAGCAG 1680  
Db TATGATTTCTTAAACATCACTGCAATAGAGGTTGAATTAATAAATTTTCAATGTTGAGCAG 1680  
Qy AAATATTCATTTTACAGTGTAAATGAGTCCCAGCCATGTTGTCACATGTTCAAGCCC 1740  
Db AAATATTCATTTTACAGTGTAAATGAGTCCCAGCCATGTTGTCACATGTTCAAGCCC 1740  
Qy CAAAGGAGAGACAGCGGAAACAAGTCTTTTACCCTTTGATATTTTGCATTTAGTGGGAGA 1800  
Db CAAAGGAGAGACAGCGGAAACAAGTCTTTTACCCTTTGATATTTTGCATTTAGTGGGAGA 1800  
Qy GATGCAATTAAGCAATAGCAGAGAAAGATATACATCAGGAAATCATGGGTGTTGTA 1860  
Db GATGCAATTAAGCAATAGCAGAGAAAGATATACATCAGGAAATCATGGGTGTTGTA 1860  
Qy GAAGCAGAGAAAGTCAGGGCAAGTCACTCTGGGGCTGACACTTTGAGCAGAGACATGAAGA 1920  
Db GAAGCAGAGAAAGTCAGGGCAAGTCACTCTGGGGCTGACACTTTGAGCAGAGACATGAAGA 1920  
Qy AATAAGAAATGATTTGACTGGGAGCAGTATTTTCCAGGCAAACTGAGTGGGCTGGCAAG 1980  
Db AATAAGAAATGATTTGACTGGGAGCAGTATTTTCCAGGCAAACTGAGTGGGCTGGCAAG 1980  
Qy TTGGATTTAAAGACGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040  
Db TTGGATTTAAAGACGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040  
Qy CGGCGTGGGGTGGGAAGGGGACTTACCATCTGCAATGAGGATGCTAGCAGTATCTCTGT 2100  
Db CGGCGTGGGGTGGGAAGGGGACTTACCATCTGCAATGAGGATGCTAGCAGTATCTCTGT 2100  
Qy CCTCCCTACTCTACTAGGTGCTAGGAGCACTCCCCCAGTCTTGACAAACCAAAAATGTCTCT 2160  
Db CCTCCCTACTCTACTAGGTGCTAGGAGCACTCCCCCAGTCTTGACAAACCAAAAATGTCTCT 2160  
Qy AAATTTTGGCAATGCTAGTACAAAATCTCTGGTTAAGAAAGCTCGGGTTGAAAAA 2220  
Db AAATTTTGGCAATGCTAGTACAAAATCTCTGGTTAAGAAAGCTCGGGTTGAAAAA 2220  
Qy AATAAACAGTAGTCTGGGAGTAGGCCAAGAGTAGGTAAATGGGCTCAGAGAGGA 2280  
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Qy GCCCAAAACAGGTTGTGCGAGCGCCTGTAGGCTGTGGTGTGAAATTTCTAGCCAAAGGTA 2340

Db 2281 GCCCAAAACAGGTTGTGCGAGCGCCTGTAGGCTGTGGTGTGAAATTTCTAGCCAAAGGTA 2340  
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Db ACAGTGATCTCTCACAGGCTTTTAAAGATTTGCTCTGGCTGTATGTGGAAGCAGAATG 2400  
Qy AAGGAGCAACACAGTAAAGACAGGAGCCAGCCAGGAAGCTGTTACACAGTCCAGGCAAG 2460  
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Qy AGGTAGTGGAGTGGGCTGGGTAACAGAAAAGGAGTGAACAAACCAATTTCTCTGAA 2520  
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Qy TATATTTCTGAAGGAAGTTGCTGAAGGATTTCTATGTTGTGTGAGAGAAAGAAATTTGG 2580  
Db TATATTTCTGAAGGAAGTTGCTGAAGGATTTCTATGTTGTGTGAGAGAAAGAAATTTGG 2580  
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Qy GTTCAAGACCAAGCTTGGGCAACACAGCAAAACCCCTTCTCTACAAAATAACAAAAATTA 2700  
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Qy GCTGGTGTGTGGCATGCACTGTGATCTCTAGCTACTCGGGAGGCTGAGGTGGAGGTA 2760  
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Qy TTGCTTGAGCCAGGAAGTTGAGGCTGAGGCAATGACTGTGCCACTGTACTTTCAGC 2820  
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Qy CTAGGTGACAGAGCAAGACCCCTGTCTCCCTGACCCCTGAAAAAGAGAGATTTAAAGT 2880  
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Db TTGAGTCCAGGTTTTCAGGAGCTTAGTGAGGAATCCCTTTGAACCCAGGAGGTGCAGG 3360  
Qy CTCAAAAAAATTTTCTAGGATTTGGG 3420  
Db CTCAAAAAAATTTTCTAGGATTTGGG 3420



QY 3421 TCTAATTTGGCCCTGAGCACCACCACTCTCTGAGTTCAACTACCATGGCTAGACACACCTTTAAC 3480  
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 QY 3781 CCTCTTCATGGGTGCTCAGAGCAGGACCTTGGTCTTTTCTTGTGTTGAAGCTTTGGGCTA 3840  
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 QY 4501 GACCAACAAGGATATGGTGGAAACACACACTTCTGCCCTATATCTAGTGGCAGAGTGGAGG 4560  
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 QY 4561 AGGTTGCAGGGACCGGAATCCCTGGTTGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC 4620  
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 QY 4561 AGGTTGCAGGGACCGGAATCCCTGGTTGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC 4620  
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 QY 4621 TCCAAATTCCTGGGAAAGGACTTTTCAATCCCTAGAGTCTCTACCTTATAATTGAGATGTA 4680  
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 QY 4681 TGAGCAGCAGCACAAGTCATGGGTTTAAATTTCTTCTCCATGCATATGGCTCAAAAGGAA 4740  
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 QY 4741 GTGTCTATGGCCCTTGTCTTTTATTTAACCAATAATCTTTTGTATATTTATACCTGTTAA 4800  
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 QY 4801 AATTTTCAGAAATGTCAAGCCGGGACGCTGCTCAACCTGTAATCCAGCAGCTTTGGG 4860  
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 QY 4861 AGGCCGAGCGGGTGGTCAACAAGGTCAGGAGTTTGAGACAGCCTGACCAACATGTTGAA 4920  
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 QY 4921 ACCCGTCTCTAAAAAATACAAAAATTTAGCTGGTCAGTCAATGCGCAGCTGTGTAGTCCCA 4980  
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 QY 4981 GCTAATTTGGAAGCTGAGGC 5000  
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 QY 4981 GCTAATTTGGAAGCTGAGGC 5000  
 Db |||||

RESULT 6  
 AAC68427  
 ID AAC68427 standard; DNA; 10825 BP.  
 XX AC AAC68427;  
 XX DT 21-FEB-2001 (first entry)  
 XX DE Human hereditary hemochromatosis 24d2 mutation DNA.  
 XX HH; hereditary hemochromatosis; chelation agent;  
 KW T-cell differentiation factor; iron overload; ds.  
 XX OS Homo sapiens.  
 XX PN US6140305-A.  
 XX PD 31-OCT-2000.  
 XX PF 04-APR-1997; 97US-00834497.  
 XX PR 04-APR-1996; 96US-00630912.  
 PR 16-APR-1996; 96US-00632673.  
 PR 23-MAY-1996; 96US-00652265.  
 XX PA (BIRA ) BIO-RAD LAB INC.  
 XX PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Teuchihaashi Z, Wolff RK;  
 PI Feder JN;  
 XX DR WPI; 2001-006341/01.  
 DR P-PSDB; AAB36871.  
 XX PT New hereditary hemochromatosis gene products or polypeptides, useful for  
 PT treating hereditary hemochromatosis in a patient, and as a metal  
 PT chelation agent alleviating iron overload.



XX	Disclosure; Fig 3; 108pp; English.	
PS	The present invention relates to hereditary hemochromatosis gene products. These proteins may be used to treat a patient diagnosed as having human hemochromatosis disease. It is also useful as a metal chelation agent or as a T-cell differentiation factor, and for alleviating iron overload. They may also be used in protein replacement therapy for individuals having a defective human hemochromatosis gene	
XX	Sequence 10825 BP; 2998 A; 2252 C; 2649 G; 2926 T; 0 U; 0 Other;	
SQ	Query Match 100.0%; Score 4998.4; DB 5; Length 10825; Best Local Similarity 100.0%; Pred. No. 0; Matches 4999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 TCTAAGGTTGAGATAAAATTTTAAATGATGATGAAATTTTGAATAATCATAAATATTTA 60	841 AAGTTCTTCCCTGAGTGCTTGCCGGAAGGCTGAGCAAAACCAACAGCAGGATCCGACCG 900
DB	1 TCTAAGGTTGAGATAAAATTTTAAATGATGATGAAATTTTGAATAATCATAAATATTTA 60	
QY	61 AATATCTAAAGTTTCAGATCAGAACATATGCGAAGCTACTTTCCCAATCAACACCCCT 120	901 G3TTTCCACCTCAGAACGAATCGTTGGCGCGTGGGGCGCGAAAGAGTGGCGTTGGGA 960
DB	61 AATATCTAAAGTTTCAGATCAGAACATATGCGAAGCTACTTTCCCAATCAACACCCCT 120	901 G3TTTCCACCTCAGAACGAATCGTTGGCGCGTGGGGCGCGAAAGAGTGGCGTTGGGA 960
QY	121 TCAGGATTTAAACCAAGGGGGACATGCGATCACTAGTGTTTCAAGCAGAGTACCTT 180	961 TCTGAATTTCTTCAACATTTCCACCCACTTTTGGTGAGACCTGGGGTGGAGGTTCTTAGG 1020
DB	121 TCAGGATTTAAACCAAGGGGGACATGCGATCACTAGTGTTTCAAGCAGAGTACCTT 180	961 TCTGAATTTCTTCAACATTTCCACCCACTTTTGGTGAGACCTGGGGTGGAGGTTCTTAGG 1020
QY	181 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTGTCTTTTCAACAGGAAGTT 240	1021 GGGAGGCTCTGAGAGAGGCTTACCTCGGGCTTTTCCCACTCTTTGGCAATTTGTTCTTTT 1080
DB	181 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTGTCTTTTCAACAGGAAGTT 240	1021 GGGAGGCTCTGAGAGAGGCTTACCTCGGGCTTTTCCCACTCTTTGGCAATTTGTTCTTTT 1080
QY	241 TTAATGCGGATCTCTGAGCTAGGCAATAGCTGTAGGGTGACTTTGAGAGCATCCCG 300	1081 GCCTGGAAAAATTAAGTATATGTTAGTTTGAACGTTTGAACCTGAACAATTTCTCTTTTCGG 1140
DB	241 TTAATGCGGATCTCTGAGCTAGGCAATAGCTGTAGGGTGACTTTGAGAGCATCCCG 300	1081 GCCTGGAAAAATTAAGTATATGTTAGTTTGAACGTTTGAACCTGAACAATTTCTCTTTTCGG 1140
QY	301 TTTTCCCGCCCCCAAGAGCGAGATTTAACGGGACGTCGGCCAGAGCTCGGGAA 360	1141 CTAGGCTTTATGATTGCAATGCTGTGTAAATTAAGAGGCTCTCTACAAAGTACTGA 1200
DB	301 TTTTCCCGCCCCCAAGAGCGAGATTTAACGGGACGTCGGCCAGAGCTCGGGAA 360	1141 CTAGGCTTTATGATTGCAATGCTGTGTAAATTAAGAGGCTCTCTACAAAGTACTGA 1200
QY	361 ATGGGCGCGAGCCAGGCGCGCTTCTCTCTGATGCTTTTGCAGACCGCGTCTGT 420	1201 TAAATGAAATGTAAGCAATGCACCTCTTAAAGTTACATTCATATCTGATCTTATTTGA 1260
DB	361 ATGGGCGCGAGCCAGGCGCGCTTCTCTCTGATGCTTTTGCAGACCGCGTCTGT 420	1201 TAAATGAAATGTAAGCAATGCACCTCTTAAAGTTACATTCATATCTGATCTTATTTGA 1260
QY	421 CAGGGCGCTTCTGCTGAGTCGAGGCTCGGGCGAACTAGGGGCGCGCGGGGTG 480	1261 TTTTCACTAGGAGAGGAGTAACTCTTTTCAAGTTTCAAGAAACAATAAATCTGTTTCTG 1380
DB	421 CAGGGCGCTTCTGCTGAGTCGAGGCTCGGGCGAACTAGGGGCGCGCGGGGTG 480	1261 TTTTCACTAGGAGAGGAGTAACTCTTTTCAAGTTTCAAGAAACAATAAATCTGTTTCTG 1380
QY	481 GAAAAATCGAACTAGCTTTTCTTGGCTTTGGGAGTTTGTAACTTTGGAGGACCTGC 540	1381 ATGTTATTTTCAAGTACTACAGCTCTTCTTAACTTTAGTTTGAAGTGAATTTTGGCCCTGTAG 1440
DB	481 GAAAAATCGAACTAGCTTTTCTTGGCTTTGGGAGTTTGTAACTTTGGAGGACCTGC 540	1381 ATGTTATTTTCAAGTACTACAGCTCTTCTTAACTTTAGTTTGAAGTGAATTTTGGCCCTGTAG 1440
QY	541 TCAACCTATCCGCAAGCCCTCTCCCTACTTTCTGGTCCAGACCCCGTGGAGGTGC 600	1441 TGTAGCAGAGTGTCTGTGGGTCAACGCCGCGCTTCAGCAGCAGCTTTGAGTTTGGTA 1500
DB	541 TCAACCTATCCGCAAGCCCTCTCCCTACTTTCTGGTCCAGACCCCGTGGAGGTGC 600	1441 TGTAGCAGAGTGTCTGTGGGTCAACGCCGCGCTTCAGCAGCAGCTTTGAGTTTGGTA 1500
QY	601 CTACACATGAACTAGAGGTCTCTGGCCAGAGCTCTGCCCCCTCCCGGCTGT 660	1501 CTACGTGTATCCACATTTTACATGACAAAGATGAGGATGAGGATGAGGATGAGGATGAGG 1560
DB	601 CTACACATGAACTAGAGGTCTCTGGCCAGAGCTCTGCCCCCTCCCGGCTGT 660	1501 CTACGTGTATCCACATTTTACATGACAAAGATGAGGATGAGGATGAGGATGAGGATGAGG 1560
QY	661 CCGGCTCTGGGAGTGACTTTTGAACCGCCACTTCCCTTCCCACTAGAAATGCTTT 720	1561 CAAATTTTATCAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGCTCTCCACTTCATAGC 1620
DB	661 CCGGCTCTGGGAGTGACTTTTGAACCGCCACTTCCCTTCCCACTAGAAATGCTTT 720	1561 CAAATTTTATCAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGCTCTCCACTTCATAGC 1620
QY	721 TAAATAAATCTCGTAGTTCTTCACTTGAAGCTAGCTAGGCTTGGGCTCTTTGAACCTGG 780	1621 TATGATTTCTTAAACATCACTGCAATTAAGAGTTGAATTAATAATTTCTAGTTGAGCAG 1680
DB	721 TAAATAAATCTCGTAGTTCTTCACTTGAAGCTAGCTAGGCTTGGGCTCTTTGAACCTGG 780	1621 TATGATTTCTTAAACATCACTGCAATTAAGAGTTGAATTAATAATTTCTAGTTGAGCAG 1680
QY	781 AACTCGGGTTTATTTTCAATGTCAGCTGTGAGTGTCTTTTCCCACTGATCTCCAAACAGG 840	1681 AAATTTTCAATTTTGAAGTGAATGAGTCCAGCCCATGTTGTCATGTTTCAAGCCC 1740
DB	781 AACTCGGGTTTATTTTCAATGTCAGCTGTGAGTGTCTTTTCCCACTGATCTCCAAACAGG 840	1681 AAATTTTCAATTTTGAAGTGAATGAGTCCAGCCCATGTTGTCATGTTTCAAGCCC 1740
QY	841 AAGTTCTTCCCTGAGTGCTTGCCGGAAGGCTGAGCAAAACCAACAGCAGGATCCGACCG 900	1741 CAAAGGAGAGAGCAGGGGAAAACAAGTCTTTTCCCTTTGATATTTTGTGATATTTTGTGAGG 1800
		1741 CAAAGGAGAGAGCAGGGGAAAACAAGTCTTTTCCCTTTGATATTTTGTGATATTTTGTGAGG 1800
		1801 GATGACAAATGAAGAAATGAGCAGAAAGATATACAACTCAGGAATCATGGGTGTTTGA 1860
		1801 GATGACAAATGAAGAAATGAGCAGAAAGATATACAACTCAGGAATCATGGGTGTTTGA 1860
		1861 GAAGCAGAGAGTCAAGGCAAGTCACTCTGGGCTGACACTTGACGAGACATCAAGGA 1920
		1861 GAAGCAGAGAGTCAAGGCAAGTCACTCTGGGCTGACACTTGACGAGACATCAAGGA 1920
		1921 AATGAAGATGATATTTGACTGGGAGCAGTATTTTCCAGGCAAACTGAGTGGGCTCGGCAAG 1980







QY 4141 GAATTTGCTTCTGAGATCAATTTGGTCTCTTGGGATGGTGAATAGGACCTATTCCTT 4200  
Db |||||  
QY 4141 GAATTTGCTTCTGAGATCAATTTGGTCTCTTGGGATGGTGAATAGGACCTATTCCTT 4200  
Db |||||  
QY 4201 TGGTTGCAGTTAAACAGGCTGGGATTTTTCCAGAGTCCACACCTGCAAGTCAATCCTG 4260  
Db |||||  
QY 4201 TGGTTGCAGTTAAACAGGCTGGGATTTTTCCAGAGTCCACACCTGCAAGTCAATCCTG 4260  
Db |||||  
QY 4261 GGCTGTGAATGCAAGAGAACAGTACCGAGGCTACTGGAAGTACGGGTATGATGGG 4320  
Db |||||  
QY 4261 GGCTGTGAATGCAAGAGAACAGTACCGAGGCTACTGGAAGTACGGGTATGATGGG 4320  
Db |||||  
QY 4321 CAGGACCACTTGAATCTGCCCTGCACACCTGGATTCGAGAGCAGACCCAGGGCC 4380  
Db |||||  
QY 4321 CAGGACCACTTGAATCTGCCCTGCACACCTGGATTCGAGAGCAGACCCAGGGCC 4380  
Db |||||  
QY 4381 TGGCCCAACCAAGCTGGAGTGGGAAGGACAAAGATTCGGGGCCAGGACAGAGCGGCTAC 4440  
Db |||||  
QY 4381 TGGCCCAACCAAGCTGGAGTGGGAAGGACAAAGATTCGGGGCCAGGACAGAGCGGCTAC 4440  
Db |||||  
QY 4441 CTGGAGAGGAGTGCCTCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGAGAGGTGTTTG 4500  
Db |||||  
QY 4441 CTGGAGAGGAGTGCCTCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGAGAGGTGTTTG 4500  
Db |||||  
QY 4501 GACCAACAGGTATGGTGAACACACTTCTGCCCTTACTCTAGTGGCAGAGTGGAGG 4560  
Db |||||  
QY 4501 GACCAACAGGTATGGTGAACACACTTCTGCCCTTACTCTAGTGGCAGAGTGGAGG 4560  
Db |||||  
QY 4561 AGGTTGTCAGGGCAGCGAATCCCTGGTTGAGTTCAGAGGTGGCTGAGGCTGTGCTC 4620  
Db |||||  
QY 4561 AGGTTGTCAGGGCAGCGAATCCCTGGTTGAGTTCAGAGGTGGCTGAGGCTGTGCTC 4620  
Db |||||  
QY 4621 TCCAAATCTCGGAAGGAGCTTTCTCAATCCTAGAGTCTTACCTTATAATGAGATGTA 4680  
Db |||||  
QY 4621 TCCAAATCTCGGAAGGAGCTTTCTCAATCCTAGAGTCTTACCTTATAATGAGATGTA 4680  
Db |||||  
QY 4681 TCAGACAGCCAGTCAATGGGTTAAATTTCTCCATGCATATGCTCAAGGGAA 4740  
Db |||||  
QY 4681 TCAGACAGCCAGTCAATGGGTTAAATTTCTCCATGCATATGCTCAAGGGAA 4740  
Db |||||  
QY 4741 GTGCTATGCGCCTGCTTTTATTTAAACCAATATCTTTTGTATATTTATACCTGTAA 4800  
Db |||||  
QY 4801 AAATTCAGAAATGTCAAGCCGGGACGCTGCTCAACCTGTATCCAGACACTTTGGG 4860  
Db |||||  
QY 4801 AAATTCAGAAATGTCAAGCCGGGACGCTGCTCAACCTGTATCCAGACACTTTGGG 4860  
Db |||||  
QY 4861 AGGCGAGGCGGTGTCAAGGTTCAGAGTTCAGAGCCAGCCTGACCAATGCTGAA 4920  
Db |||||  
QY 4861 AGGCGAGGCGGTGTCAAGGTTCAGAGTTCAGAGCCAGCCTGACCAATGCTGAA 4920  
Db |||||  
QY 4921 ACCCGTCTCTAAAAAATAAAAAATAGCTGGTCAAGTCAATGCGCAGCTAGTCCCA 4980  
Db |||||  
QY 4921 ACCCGTCTCTAAAAAATAAAAAATAGCTGGTCAAGTCAATGCGCAGCTAGTCCCA 4980  
Db |||||  
QY 4981 GCTAATTTGAAGGCTGAGGC 5000  
Db |||||  
QY 4981 GCTAATTTGAAGGCTGAGGC 5000  
Db |||||

RESULT 7

AAC68428  
ID AAC68428 standard; DNA; 10825 BP.  
XX  
AC AAC68428;  
XX  
XX 21-FEB-2001 (first entry)  
DT  
XX Human hereditary hemochromatosis 24d1/2 mutation DNA.  
DE  
XX HH; hereditary hemochromatosis; chelation agent;  
KW  
KW T-cell differentiation factor; iron overload; ds.

XX Homo sapiens.  
OS US6140305-A.  
XX  
PN 31-OCT-2000.  
XX  
XX 04-APR-1997; 97US-00834497.  
XX  
XX 04-APR-1996; 96US-00630912.  
PR 16-APR-1996; 96US-00632673.  
PR 23-MAY-1996; 96US-00652265.  
XX  
XX (BIRA ) BIO-RAD LAB INC.  
PA  
PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Teuchihaishi Z, Wolff RK;  
PI Feder JN;  
XX  
XX WPI; 2001-006341/01.  
DR P-PSDB; AAB36872.  
XX  
XX New hereditary hemochromatosis gene products or polypeptides, useful for  
PT treating hereditary hemochromatosis in a patient, and as a metal  
PT chelation agent alleviating iron overload.  
XX  
XX Disclosure; Fig 3; 108pp; English.  
XX  
CC The present invention relates to hereditary hemochromatosis gene  
CC products. These proteins may be used to treat a patient diagnosed as  
CC having human hemochromatosis disease. It is also useful as a metal  
CC chelation agent or as a T-cell differentiation factor, and for  
CC alleviating iron overload. They may also be used in protein replacement  
CC therapy for individuals having a defective human hemochromatosis gene  
XX  
SQ Sequence 10825 BP; 2999 A; 2252 C; 2648 G; 2926 T; 0 U; 0 Other;

Query Match 100.0%; Score 4998.4; DB 5; Length 10825;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 TCTAAGGTGAGATAAAATTTTAAATGATGATGAAATTTTGAATAATATTTA 60  
Db |||||  
1 TCTAAGGTGAGATAAAATTTTAAATGATGATGAAATTTTGAATAATATTTA 60  
QY 61 AATATCTAAAGTTCAGATCAGAACATTCGGAAGCTACTTCCCAATCAACACACCCCT 120  
Db |||||  
61 AATATCTAAAGTTCAGATCAGAACATTCGGAAGCTACTTCCCAATCAACACACCCCT 120  
QY 121 TCAGGATTTAAAAACCAAGGGGACACCTGGATCACCTAGTGTTCACAAGCAGGTACCTT 180  
Db |||||  
121 TCAGGATTTAAAAACCAAGGGGACACCTGGATCACCTAGTGTTCACAAGCAGGTACCTT 180  
QY 181 CTGCTGTAGGAGAGAGAGAACTAAAGTTCTGAAAGACCTGTGCTTTTCCACAGGAAGTT 240  
Db |||||  
181 CTGCTGTAGGAGAGAGAGAACTAAAGTTCTGAAAGACCTGTGCTTTTCCACAGGAAGTT 240  
QY 241 TTACTGGGCATCTCCTGAGCCTTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCCG 300  
Db |||||  
241 TTACTGGGCATCTCCTGAGCCTTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCCG 300  
QY 301 TTTCCCGCCCCCAAAAGAGAGCGAGATTTAAACGGGACGTCGGCCAGAGCTGGGAA 360  
Db |||||  
301 TTTCCCGCCCCCAAAAGAGAGCGAGATTTAAACGGGACGTCGGCCAGAGCTGGGAA 360  
QY 361 ATGGGCCCGCAGGACGAGCCGCGCTTCTCTCTGATGCTTTTTCAGACCGCGGTCTCG 420  
Db |||||  
361 ATGGGCCCGCAGGACGAGCCGCGCTTCTCTCTGATGCTTTTTCAGACCGCGGTCTCG 420  
QY 421 CAGGGCCGCTTCTGCTGAGTCCGAGGCTCGCGGCGAATAGGGGCGCGCGGGGTG 480  
Db |||||  
421 CAGGGCCGCTTCTGCTGAGTCCGAGGCTCGCGGCGAATAGGGGCGCGCGGGGTG 480  
QY 481 GAAAAATCGAAACTAGCTTTTCTTTGGCTTGGGAGTTTGTCTAACTTTGGAGGACCTGC 540



Db 481 GAAAAATCGAAACTAGCTTTTCTTTTGGCGCTGGAGTTTGTCTAACTTTTGGAGGACCTGC 540  
Qy 541 TCAACCTATTCGCAAGCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGGAGTGC 600  
Db 541 TCAACCTATTCGCAAGCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGGAGTGC 600  
Qy 601 CTACCACTGAATGCAATGAGGGTCCCTCGCCCCCAGGACCTGCCCCCTCCCCCGGCTGT 660  
Db 601 CTACCACTGAATGCAATGAGGGTCCCTCGCCCCCAGGACCTGCCCCCTCCCCCGGCTGT 660  
Qy 661 CCGGCTCTCGGAGTGAATTTTGGAAACCCCACTCCCTTCCCCCAATAGAAATGCTTT 720  
Db 661 CCGGCTCTCGGAGTGAATTTTGGAAACCCCACTCCCTTCCCCCAATAGAAATGCTTT 720  
Qy 721 TAAATAAACTCTGCTAGTCTCTCACTTGAAGTGAAGCTTAAGCTCGGGCTCCTTGAACCTGG 780  
Db 721 TAAATAAACTCTGCTAGTCTCTCACTTGAAGTGAAGCTTAAGCTCGGGCTCCTTGAACCTGG 780  
Qy 781 AACTCGGGTTTATTTCCAAATGTGAGCTGTGAGCTTTTTCCTCCAGTCACTCTCCAAACAGG 840  
Db 781 AACTCGGGTTTATTTCCAAATGTGAGCTGTGAGCTTTTTCCTCCAGTCACTCTCCAAACAGG 840  
Qy 841 AAGTTCTTCCCTGAGTGTCTGCGAGAAAGCTGAGCAAAACCACAGAGGATCCGACAGG 900  
Db 841 AAGTTCTTCCCTGAGTGTCTGCGAGAAAGCTGAGCAAAACCACAGAGGATCCGACAGG 900  
Qy 901 GGTTCCTCACCTCAGAACGAAATGCTTGGCGGTGGGGCGCGAAAGAGTGGGCTTGGGGA 960  
Db 901 GGTTCCTCACCTCAGAACGAAATGCTTGGCGGTGGGGCGCGAAAGAGTGGGCTTGGGGA 960  
Qy 961 TCTGAATTTCTCACTTCCACCACCTTTTGTGTGAGACCTGGGGTGGAGTCTCTAGGGT 1020  
Db 961 TCTGAATTTCTCACTTCCACCACCTTTTGTGTGAGACCTGGGGTGGAGTCTCTAGGGT 1020  
Qy 1021 GGGAGGCTCTGAGAGAGGCTACCTCGGGCTTTCCCACTCTTGGGCAATTTGTTCTTTT 1080  
Db 1021 GGGAGGCTCTGAGAGAGGCTACCTCGGGCTTTCCCACTCTTGGGCAATTTGTTCTTTT 1080  
Qy 1081 GCTCGAAATTAAGTATATGTTAGTTTGAACGTTTGAACGAAATTTCTCTTTTCGG 1140  
Db 1081 GCTCGAAATTAAGTATATGTTAGTTTGAACGTTTGAACGAAATTTCTCTTTTCGG 1140  
Qy 1141 CTAGGCTTTATGATTTGCAATGCTGTGTAAATTAAGAGGCTCTCTACAAAGTACTGA 1200  
Db 1141 CTAGGCTTTATGATTTGCAATGCTGTGTAAATTAAGAGGCTCTCTACAAAGTACTGA 1200  
Qy 1201 TAATGAACATGTAAGCAATGCACTCTTAAGTTTACATTTCAATCTCTATTTGA 1260  
Db 1201 TAATGAACATGTAAGCAATGCACTCTTAAGTTTACATTTCAATCTCTATTTGA 1260  
Qy 1261 TTTTCACTAGGCATAGGAGGTAGGAGCTAAATAACGTTTATTTTACTAGAGTTAACT 1320  
Db 1261 TTTTCACTAGGCATAGGAGGTAGGAGCTAAATAACGTTTATTTTACTAGAGTTAACT 1320  
Qy 1321 GGAATTCAGATTAATAAATCTTTTTCAGGTTTCAAAAGAACATAAATAAATCTGTTTCTG 1380  
Db 1321 GGAATTCAGATTAATAAATCTTTTTCAGGTTTCAAAAGAACATAAATAAATCTGTTTCTG 1380  
Qy 1381 ATGTTATTTCAAGTACTAGAGTGTCTTAAATCTTTAGTTTGAAGTGAATTTGCCCCGTAG 1440  
Db 1381 ATGTTATTTCAAGTACTAGAGTGTCTTAAATCTTTAGTTTGAAGTGAATTTGCCCCGTAG 1440  
Qy 1441 TGTAGCACAGTGTCTGTTGGGTTCACACGCGGCTCAGCACAGCACTTTTGAAGTTTGGTA 1500  
Db 1441 TGTAGCACAGTGTCTGTTGGGTTCACACGCGGCTCAGCACAGCACTTTTGAAGTTTGGTA 1500  
Qy 1501 CTACGTGTATCCACATTTTACACATGACAAAGATGAGGCATGCGACGGCTGCTCCCTGG 1560  
Db 1501 CTACGTGTATCCACATTTTACACATGACAAAGATGAGGCATGCGACGGCTGCTCCCTGG 1560  
Qy 1561 CAAATTTATCAATGTGACATGCGGCTTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620  
Db 1561 CAAATTTATCAATGTGACATGCGGCTTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620  
Qy 1621 TATGATTTCTTAAACATCACAATGAGTTGAGTTGAAATTAATAAATTTTCAATGTTAGCAG 1680  
Db 1621 TATGATTTCTTAAACATCACAATGAGTTGAGTTGAAATTAATAAATTTTCAATGTTAGCAG 1680  
Qy 1681 AATATTTCAATGTTTAAAGTGTAAATGAGTCCCACCATGTTGTCACATGTTTCAAGCCC 1740  
Db 1681 AATATTTCAATGTTTAAAGTGTAAATGAGTCCCACCATGTTGTCACATGTTTCAAGCCC 1740  
Qy 1741 CAAAGGAGAGAGAGAGGAAACAAAGTCTTTTACCTTTTGAATATTTTGGCAATCTAGTGGAGA 1800  
Db 1741 CAAAGGAGAGAGAGAGGAAACAAAGTCTTTTACCTTTTGAATATTTTGGCAATCTAGTGGAGA 1800  
Qy 1801 GATGACAAATAGCAATAGAGAGAGATATACATCAGGAAATCATGGGTGTTGTGA 1860  
Db 1801 GATGACAAATAGCAATAGAGAGAGATATACATCAGGAAATCATGGGTGTTGTGA 1860  
Qy 1861 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGGCTGACACTTTGAGCAGAGACATGAAGGA 1920  
Db 1861 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGGCTGACACTTTGAGCAGAGACATGAAGGA 1920  
Qy 1921 AATAAGAAATGATTTGACATGAGGAGAGATTTTCCAGGCAAACTGAGTGGGCTGCGAAG 1980  
Db 1921 AATAAGAAATGATTTGACATGAGGAGAGATTTTCCAGGCAAACTGAGTGGGCTGCGAAG 1980  
Qy 1981 TTTGGATTTAAAGACGGGTTTTCTCAGCACTACTCATGTGTGTGTGGGGGGGGGG 2040  
Db 1981 TTTGGATTTAAAGACGGGTTTTCTCAGCACTACTCATGTGTGTGTGGGGGGGGGG 2040  
Qy 2041 CCGCGTGGGGTGGGAAGGGGACCTACCATCTGCACTGTAGGATGTCTAGCAGTATCTCTGT 2100  
Db 2041 CCGCGTGGGGTGGGAAGGGGACCTACCATCTGCACTGTAGGATGTCTAGCAGTATCTCTGT 2100  
Qy 2101 CCTCCCTACTCACTAGTGTCTAGGAGCACTCCCGCAGCTTGTGACAAACCAAAATGTCTCT 2160  
Db 2101 CCTCCCTACTCACTAGTGTCTAGGAGCACTCCCGCAGCTTGTGACAAACCAAAATGTCTCT 2160  
Qy 2161 AAACCTTTGCAATGTCACCTAGTAGACAAATCTCTGGTTAAGAGCTCGGGTTGAAAAA 2220  
Db 2161 AAACCTTTGCAATGTCACCTAGTAGACAAATCTCTGGTTAAGAGCTCGGGTTGAAAAA 2220  
Qy 2221 AATAAACAAAGTGTCTGGGAGTAGAGGCCAAGAAAGTAGTAAATGGGCTCAGAAAGAGA 2280  
Db 2221 AATAAACAAAGTGTCTGGGAGTAGAGGCCAAGAAAGTAGTAAATGGGCTCAGAAAGAGA 2280  
Qy 2281 GCCCAAAACAAAGTTGTGAGGCGCTGTAGGCTGTGGTGTGAAATTTCTAGCCAAAGAGTA 2340  
Db 2281 GCCCAAAACAAAGTTGTGAGGCGCTGTAGGCTGTGGTGTGAAATTTCTAGCCAAAGAGTA 2340  
Qy 2341 ACAGTGTCTGTACAGGCTTTTAAAGATTTCTCTGGCTGTCTATGTGTGAAAGAGCAATG 2400  
Db 2341 ACAGTGTCTGTACAGGCTTTTAAAGATTTCTCTGGCTGTCTATGTGTGAAAGAGCAATG 2400  
Qy 2401 AAGGAGCAACAAAGTAAAAAGCAGGAGCCAGCAGGAAAGCTTTTACACAGTCCAGGCAAG 2460  
Db 2401 AAGGAGCAACAAAGTAAAAAGCAGGAGCCAGCAGGAAAGCTTTTACACAGTCCAGGCAAG 2460  
Qy 2461 AGGTAGTGTGAGTGGGCTGGTGGGAAACAGAAAGGAGTGAACAAACCAATTTCTCTGAA 2520  
Db 2461 AGGTAGTGTGAGTGGGCTGGTGGGAAACAGAAAGGAGTGAACAAACCAATTTCTCTGAA 2520  
Qy 2521 TATATTTCTGAAGGAATTTGCTGAAGATTTCTATGTTGTGTGAGAAAGAGAAATTCG 2580  
Db 2521 TATATTTCTGAAGGAATTTGCTGAAGATTTCTATGTTGTGTGAGAAAGAGAAATTCG 2580  
Qy 2581 CTGGGTGTAGTGTCTCATGCCAAGGAGGCCAAGGAGCAGATTTCTCTAGCTCAGGA 2640  
Db 2581 CTGGGTGTAGTGTCTCATGCCAAGGAGGCCAAGGAGCAGATTTCTCTAGCTCAGGA 2640  
Qy 2641 GTTCAAGACCAAGCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAAATACAAAAATTA 2700  
Db 2641 GTTCAAGACCAAGCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAAATACAAAAATTA 2700

Db 1561 CAAATTTATTAATGTGTACATGCGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620  
Qy 1621 TATGATTTCTTAAACATCACAATGAGTTGAAATTAATAAATTTTCAATGTTAGCAG 1680  
Db 1621 TATGATTTCTTAAACATCACAATGAGTTGAAATTAATAAATTTTCAATGTTAGCAG 1680  
Qy 1681 AATATTTCAATGTTTAAAGTGTAAATGAGTCCCACCATGTTGTCACATGTTTCAAGCCC 1740  
Db 1681 AATATTTCAATGTTTAAAGTGTAAATGAGTCCCACCATGTTGTCACATGTTTCAAGCCC 1740  
Qy 1741 CAAAGGAGAGAGAGAGGAAACAAAGTCTTTTACCTTTTGAATATTTTGGCAATCTAGTGGAGA 1800  
Db 1741 CAAAGGAGAGAGAGAGGAAACAAAGTCTTTTACCTTTTGAATATTTTGGCAATCTAGTGGAGA 1800  
Qy 1801 GATGACAAATAGCAATAGAGAGAGATATACATCAGGAAATCATGGGTGTTGTGA 1860  
Db 1801 GATGACAAATAGCAATAGAGAGAGATATACATCAGGAAATCATGGGTGTTGTGA 1860  
Qy 1861 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGGCTGACACTTTGAGCAGAGACATGAAGGA 1920  
Db 1861 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGGCTGACACTTTGAGCAGAGACATGAAGGA 1920  
Qy 1921 AATAAGAAATGATTTGACATGAGGAGAGATTTTCCAGGCAAACTGAGTGGGCTGCGAAG 1980  
Db 1921 AATAAGAAATGATTTGACATGAGGAGAGATTTTCCAGGCAAACTGAGTGGGCTGCGAAG 1980  
Qy 1981 TTTGGATTTAAAGACGGGTTTTCTCAGCACTACTCATGTGTGTGTGGGGGGGGGG 2040  
Db 1981 TTTGGATTTAAAGACGGGTTTTCTCAGCACTACTCATGTGTGTGTGGGGGGGGGG 2040  
Qy 2041 CCGCGTGGGGTGGGAAGGGGACCTACCATCTGCACTGTAGGATGTCTAGCAGTATCTCTGT 2100  
Db 2041 CCGCGTGGGGTGGGAAGGGGACCTACCATCTGCACTGTAGGATGTCTAGCAGTATCTCTGT 2100  
Qy 2101 CCTCCCTACTCACTAGTGTCTAGGAGCACTCCCGCAGCTTGTGACAAACCAAAATGTCTCT 2160  
Db 2101 CCTCCCTACTCACTAGTGTCTAGGAGCACTCCCGCAGCTTGTGACAAACCAAAATGTCTCT 2160  
Qy 2161 AAACCTTTGCAATGTCACCTAGTAGACAAATCTCTGGTTAAGAGCTCGGGTTGAAAAA 2220  
Db 2161 AAACCTTTGCAATGTCACCTAGTAGACAAATCTCTGGTTAAGAGCTCGGGTTGAAAAA 2220  
Qy 2221 AATAAACAAAGTGTCTGGGAGTAGAGGCCAAGAAAGTAGTAAATGGGCTCAGAAAGAGA 2280  
Db 2221 AATAAACAAAGTGTCTGGGAGTAGAGGCCAAGAAAGTAGTAAATGGGCTCAGAAAGAGA 2280  
Qy 2281 GCCCAAAACAAAGTTGTGAGGCGCTGTAGGCTGTGGTGTGAAATTTCTAGCCAAAGAGTA 2340  
Db 2281 GCCCAAAACAAAGTTGTGAGGCGCTGTAGGCTGTGGTGTGAAATTTCTAGCCAAAGAGTA 2340  
Qy 2341 ACAGTGTCTGTACAGGCTTTTAAAGATTTCTCTGGCTGTCTATGTGTGAAAGAGCAATG 2400  
Db 2341 ACAGTGTCTGTACAGGCTTTTAAAGATTTCTCTGGCTGTCTATGTGTGAAAGAGCAATG 2400  
Qy 2401 AAGGAGCAACAAAGTAAAAAGCAGGAGCCAGCAGGAAAGCTTTTACACAGTCCAGGCAAG 2460  
Db 2401 AAGGAGCAACAAAGTAAAAAGCAGGAGCCAGCAGGAAAGCTTTTACACAGTCCAGGCAAG 2460  
Qy 2461 AGGTAGTGTGAGTGGGCTGGTGGGAAACAGAAAGGAGTGAACAAACCAATTTCTCTGAA 2520  
Db 2461 AGGTAGTGTGAGTGGGCTGGTGGGAAACAGAAAGGAGTGAACAAACCAATTTCTCTGAA 2520  
Qy 2521 TATATTTCTGAAGGAATTTGCTGAAGATTTCTATGTTGTGTGAGAAAGAGAAATTCG 2580  
Db 2521 TATATTTCTGAAGGAATTTGCTGAAGATTTCTATGTTGTGTGAGAAAGAGAAATTCG 2580  
Qy 2581 CTGGGTGTAGTGTCTCATGCCAAGGAGGCCAAGGAGCAGATTTCTCTAGCTCAGGA 2640  
Db 2581 CTGGGTGTAGTGTCTCATGCCAAGGAGGCCAAGGAGCAGATTTCTCTAGCTCAGGA 2640  
Qy 2641 GTTCAAGACCAAGCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAAATACAAAAATTA 2700  
Db 2641 GTTCAAGACCAAGCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAAATACAAAAATTA 2700



Qy	2701	GCTGGGTGTGGTGGCATGCACTGTGTGATCCTAGTACTCGGAGGCTGAGGTGGAGGGTA	2760
Db	2701	GCTGGGTGTGGTGGCATGCACTGTGTGATCCTAGTACTCGGAGGCTGAGGTGGAGGGTA	2760
Qy	2761	TTGCTTGGAGCCAGGAAGTTGAGGCTGCAGTGGCCATGACTGTGCCACTGTACTTTCAGC	2820
Db	2761	TTGCTTGGAGCCAGGAAGTTGAGGCTGCAGTGGCCATGACTGTGCCACTGTACTTTCAGC	2820
Qy	2821	CTAGGTGACAGCAAGACCTGTCTCCCTGACCCCCCTGAAAAAGAGAAGAGTTAAAGT	2880
Db	2821	CTAGGTGACAGCAAGACCTGTCTCCCTGACCCCCCTGAAAAAGAGAAGAGTTAAAGT	2880
Qy	2881	TGACTTTGTTCTTTATTTATTTATTTATTTGTCCTGAGCAGTGGGTAAATGGCAATGCCAT	2940
Db	2881	TGACTTTGTTCTTTATTTATTTATTTATTTGTCCTGAGCAGTGGGTAAATGGCAATGCCAT	2940
Qy	2941	TTCTGAGATGGTGAAGCAGAGGAAGAGCAGTTTGGGGTAAATCAAGGATCTGCAATTTG	3000
Db	2941	TTCTGAGATGGTGAAGCAGAGGAAGAGCAGTTTGGGGTAAATCAAGGATCTGCAATTTG	3000
Qy	3001	GGACATGTTAAAGTTTGAGATTCCAGTCAGGCTTCCAAAGTGGTGAAGGCCACATAGGCAGATT	3060
Db	3001	GGACATGTTAAAGTTTGAGATTCCAGTCAGGCTTCCAAAGTGGTGAAGGCCACATAGGCAGATT	3060
Qy	3061	CAGTGTGAAGAAATTCAGGACCAAGGCTGGGCA CGGTGGCTCACTTCTGTAAATCCAGCACT	3120
Db	3061	CAGTGTGAAGAAATTCAGGACCAAGGCTGGGCA CGGTGGCTCACTTCTGTAAATCCAGCACT	3120
Qy	3121	TTGGTGGCTCAGGCAGGCTAGATCAATTTGAGGTGAGGAGTTTGAGACAAGCTTGGCCAAACA	3180
Db	3121	TTGGTGGCTCAGGCAGGCTAGATCAATTTGAGGTGAGGAGTTTGAGACAAGCTTGGCCAAACA	3180
Qy	3181	TGGTGAACCCCATCTGTCTACTAAATAACAAAATTAGCCCTGGTGTGGTGGCGCACGCCCT	3240
Db	3181	TGGTGAACCCCATCTGTCTACTAAATAACAAAATTAGCCCTGGTGTGGTGGCGCACGCCCT	3240
Qy	3241	ATAGTCCAGGTTTTCAGGAGGCTTAGGTTAGGAGAAATCCCTTGAAACCGAGAGGTGCAGG	3300
Db	3241	ATAGTCCAGGTTTTCAGGAGGCTTAGGTTAGGAGAAATCCCTTGAAACCGAGAGGTGCAGG	3300
Qy	3301	TTGCAGTGAAGTTGTTGGCCACTGCACCTCCAGCCCTGGGTGATAGAGTGAAGTCTGT	3360
Db	3301	TTGCAGTGAAGTTGTTGGCCACTGCACCTCCAGCCCTGGGTGATAGAGTGAAGTCTGT	3360
Qy	3361	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAACTGAAGAAATTATTCCTCAGGATTTGGG	3420
Db	3361	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAACTGAAGAAATTATTCCTCAGGATTTGGG	3420
Qy	3421	TCTAAATTTGCCCTGAGCACCAACTCCCTGAGTTCAACTACCATGGCTAGACACACCTTTAAC	3480
Db	3421	TCTAAATTTGCCCTGAGCACCAACTCCCTGAGTTCAACTACCATGGCTAGACACACCTTTAAC	3480
Qy	3481	ATTTTCTAGAAATCCACAGCTTTTAGTGGAGTCTGTCTAAATCATCAGTATTGGAAATAGGAT	3540
Db	3481	ATTTTCTAGAAATCCACAGCTTTTAGTGGAGTCTGTCTAAATCATCAGTATTGGAAATAGGAT	3540
Qy	3541	CTGGGGCAGTGAAGGGGTGGACCA CGTGTGGCAGAGAAAAAGCACACAAGGAAAGAGC	3600
Db	3541	CTGGGGCAGTGAAGGGGTGGACCA CGTGTGGCAGAGAAAAAGCACACAAGGAAAGAGC	3600
Qy	3601	ACCAGAGCTGTCTATATGGAGAGAAGACAGGACTGCAACTCACCCCTTCAAAAATGAGGA	3660
Db	3601	ACCAGAGCTGTCTATATGGAGAGAAGACAGGACTGCAACTCACCCCTTCAAAAATGAGGA	3660
Qy	3661	CCAGACACAGCTGATGGTATGAGTTGATGCAAGTGTGTGGAGCCTCAACATCTCTGCTCCC	3720
Db	3661	CCAGACACAGCTGATGGTATGAGTTGATGCAAGTGTGTGGAGCCTCAACATCTCTGCTCCC	3720
Qy	3721	CTCCTACTACATATGGTTAAGGCTGTGTCTGTCTCCAGGTTTCAACTCTCTGCACTA	3780
Db	3721	CTCCTACTACATATGGTTAAGGCTGTGTCTGTCTCCAGGTTTCAACTCTCTGCACTA	3780

Qy	3781	CCTCTTCATCGGTGCCTTCAGACGAGCACTTGTGCTCTTTCTTGTTTGAAGCTTTGGGCTA	3840
Db	3781	CCTCTTCATCGGTGCCTTCAGACGAGCACTTGTGCTCTTTCTTGTTTGAAGCTTTGGGCTA	3840
Qy	3841	CGTGGATGACCAAGCTGTTTCGTGTTCTTATGATCATGAGAGTCGCGGTGTGAGACCCCGAAC	3900
Db	3841	CGTGGATGACCAAGCTGTTTCGTGTTCTTATGATGATGAGAGTCGCGGTGTGAGACCCCGAAC	3900
Qy	3901	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA	3960
Db	3901	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA	3960
Qy	3961	AGGTTGGGATCACATGTTTCACTGTGACTTTCGGACTATTATGGAATAACAAACACAG	4020
Db	3961	AGGTTGGGATCACATGTTTCACTGTGACTTTCGGACTATTATGGAATAACAAACACAG	4020
Qy	4021	CAAGGTTATGTGAGAGGGGGCCCTCACTTCTTGAGGTTGTTCAGAGCTTTTCATCTTTTC	4080
Db	4021	CAAGGTTATGTGAGAGGGGGCCCTCACTTCTTGAGGTTGTTCAGAGCTTTTCATCTTTTC	4080
Qy	4081	ATGCATCTTCAAGGAACACGCTCGAAGTCTGAGTCTTGTGGGACGAGGGAAGGGAAG	4140
Db	4081	ATGCATCTTCAAGGAACACGCTCGAAGTCTGAGTCTTGTGGGACGAGGGAAGGGAAG	4140
Qy	4141	GAATTTGCTTCTGAGATCAATTTGGTCTTTGGGATGGTGGAAATAGGGAACATTTCCTT	4200
Db	4141	GAATTTGCTTCTGAGATCAATTTGGTCTTTGGGATGGTGGAAATAGGGAACATTTCCTT	4200
Qy	4201	TGTTTGAGTTAACAGGCTGGGGATTTTTCAGAGTCCACACCCCTGCAGGTCATCCTTG	4260
Db	4201	TGTTTGAGTTAACAGGCTGGGGATTTTTCAGAGTCCACACCCCTGCAGGTCATCCTTG	4260
Qy	4261	GGCTGTGAATTCAGGAAGACAACAGTACCGAGGCTACTTGGAAAGTACGGGTATGATGGG	4320
Db	4261	GGCTGTGAATTCAGGAAGACAACAGTACCGAGGCTACTTGGAAAGTACGGGTATGATGGG	4320
Qy	4321	CAGGACCACTTGAAATTTCTGCCCTGCACACTGGATTGGAGACGACGAAACCCAGGGCC	4380
Db	4321	CAGGACCACTTGAAATTTCTGCCCTGCACACTGGATTGGAGACGACGAAACCCAGGGCC	4380
Qy	4381	TGGGCCACCAAGCTGGAGTGGGAAAGGCAACAAGTTTGGGCCAGGCGAGAACAGGGGCTAC	4440
Db	4381	TGGGCCACCAAGCTGGAGTGGGAAAGGCAACAAGTTTGGGCCAGGCGAGAACAGGGGCTAC	4440
Qy	4441	CTGGAGAGGACCTGCCCTGCACAGCTGCACAGTGTCTGGAGCTTGGGGAGAGGTGTTTG	4500
Db	4441	CTGGAGAGGACCTGCCCTGCACAGCTGCACAGTGTCTGGAGCTTGGGGAGAGGTGTTTG	4500
Qy	4501	GACCAACAAGGTATGTGGAAACACACTTCTGCCCTTATCTCTAGTGGCAGAGTGGAGG	4560
Db	4501	GACCAACAAGGTATGTGGAAACACACTTCTGCCCTTATCTCTAGTGGCAGAGTGGAGG	4560
Qy	4561	AGTTTGAGGGCACGGAATCCCTGGTTTGGAGTTTTCAGAGTGGCTCAGGCTGTGTGCCTC	4620
Db	4561	AGTTTGAGGGCACGGAATCCCTGGTTTGGAGTTTTCAGAGTGGCTCAGGCTGTGTGCCTC	4620
Qy	4621	TCCAAATTTCTGGGAAGGACCTTCTCAATCCTAGAGTCTCTACTTATATAATTCAGATGTA	4680
Db	4621	TCCAAATTTCTGGGAAGGACCTTCTCAATCCTAGAGTCTCTACTTATATAATTCAGATGTA	4680
Qy	4681	TGAGACAGCCAAGTCATGGGTTAAATTTCTTTTTCATGTCATATGGCTCAAAAGGAA	4740
Db	4681	TGAGACAGCCAAGTCATGGGTTAAATTTCTTTTTCATGTCATATGGCTCAAAAGGAA	4740
Qy	4741	GTGTCATATGCCCTTGTCTTTTATTTAAACCAATAACTTTTGTATATTTATATCTGTATA	4800
Db	4741	GTGTCATATGCCCTTGTCTTTTATTTAAACCAATAACTTTTGTATATTTATATCTGTATA	4800
Qy	4801	AAATTCAGAAATGTCAAGGCCGGGCAACGGTGGCTCACCCCTGTAAATCCAGCACTTTGGG	4860
Db	4801	AAATTCAGAAATGTCAAGGCCGGGCAACGGTGGCTCACCCCTGTAAATCCAGCACTTTGGG	4860
Qy	4861	AGGCCGAGGGCGGTGGTTCACAAGGTGAGGATTTTGAGACACAGGCTGCACCAACATGGTAA	4920



Db 4861 AGCCGAGCGGGTGTCTCAAGGTGAGGAGTTTGAGCCAGCCTGACCAACATGCTGAA 4920  
QY 4921 ACCCGTCTCTAAAAAATACAAAAATTTAGCTGTCTACAGTCATGCGCAGCTGTAGTCCCA 4980  
Db 4921 ACCCGTCTCTAAAAAATACAAAAATTTAGCTGTCTACAGTCATGCGCAGCTGTAGTCCCA 4980  
QY 4981 GCTAATTGGAAGCTGAGGC 5000  
Db 4981 GCTAATTGGAAGCTGAGGC 5000

RESULT 8  
ADG87264  
ID ADG87264 standard; DNA; 10825 BP.  
XX AC ADG87264;  
XX DT 11-MAR-2004 (first entry)  
XX DE Hereditary haemochromatosis (HH) 24d2 mutant genomic DNA.  
XX KW Hereditary haemochromatosis; HH; inherited disorder; iron metabolism;  
XX KW cirrhosis; diabetes; illness; gene therapy; hepatotropic; mutant; gene;  
XX OS ds.  
XX OS Unidentified.

Key Location/Qualifiers  
CDS 361..7147  
FT /\*tag= b  
FT /product= "Hereditary haemochromatosis 24d2 mutant  
FT protein"  
FT exon 361..436  
FT /\*tag= a  
FT intron 437..3761  
FT /\*tag= c  
FT exon 3762..4025  
FT /\*tag= d  
FT intron 4026..4234  
FT /\*tag= e  
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FT /\*tag= i  
FT exon 6040..6153  
FT /\*tag= j  
FT intron 6154..7106  
FT /\*tag= k  
FT exon 7107..7147  
FT /\*tag= l

US2003148972-A1.  
PD 07-AUG-2003.  
XX 02-MAY-2002; 2002US-00138888.  
XX 04-APR-1996; 96US-00630912.  
XX 16-APR-1996; 96US-00632673.  
XX 23-MAY-1996; 96US-00652265.  
XX 04-APR-1997; 97US-00834497.  
XX 04-FEB-2000; 2000US-00497957.  
XX (BIRA ) BIO-RAD LAB INC.  
XX Thomas WJ, Drayna DT, .Feder JN, Gnirke A, Ruddy D, Tsuchihashi Z;  
XX Wolff RK;

DR WPI; 2003-897595/82.  
DR P-PSDB; ADG87265.  
XX  
PT New hereditary hemochromatosis (HH) nucleic acids and peptides, useful  
PT for treating HH leading to diabetes, cirrhosis, sterility or other  
PT serious illnesses.  
XX  
PS Claim 1; SEQ ID NO 5; 122pp; English.  
XX  
CC The present invention relates to gene and mutations thereto, that are  
CC responsible for the disease hereditary haemochromatosis (HH). Sequences  
CC of the invention are useful for treating hereditary haemochromatosis  
CC which is an inherited disorder or iron metabolism where the body  
CC accumulates excess iron. The excess in iron leads to cirrhosis, diabetes,  
CC and other serious illnesses. The invention is also useful in gene  
CC therapy. The present sequence is hereditary haemochromatosis 24d2 mutant  
CC genomic DNA.  
XX  
SQ Sequence 10825 BP; 2998 A; 2252 C; 2649 G; 2926 T; 0 U; 0 Other;

Query Match 100.0%; Score 4998.4; DB 10; Length 10825;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 TCTAAGGTTGAGATAAAATTTTAAATGTATGATTTGAAATTTTGAATAATCATAAATATTTA 60  
Db 1 TCTAAGGTTGAGATAAAATTTTAAATGTATGATTTGAAATTTTGAATAATCATAAATATTTA 60  
QY 61 AATATCTAAAGTTTCAGATCAGAACATTTGCGAAGCTACTTTCCCAATCAACACCCCT 120  
Db 61 AATATCTAAAGTTTCAGATCAGAACATTTGCGAAGCTACTTTCCCAATCAACACCCCT 120  
QY 121 TCAGGATTTAAACCAAGGGGACACTGATCAGTGTCTTCCAGAGAGGTACCTT 180  
Db 121 TCAGGATTTAAACCAAGGGGACACTGATCAGTGTCTTCCAGAGAGGTACCTT 180  
QY 181 CTGCTGTAGGAGAGAGAGAACTAAAGTTCTGAAAGACCTTGTCTTTTCCAGGAGGTT 240  
Db 181 CTGCTGTAGGAGAGAGAGAACTAAAGTTCTGAAAGACCTTGTCTTTTCCAGGAGGTT 240  
QY 241 TTACTGGGCACTCTCTGAGCCTTAGGCAATAGCTGTAGGTGACTTCTGAGGCAATCCCG 300  
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QY 301 TTTTCCCGCCCGCCCAAGAGCGAGATTAAACGGGACGTCGCGCAGAGCTGGGGA 360  
Db 301 TTTTCCCGCCCGCCCAAGAGCGAGATTAAACGGGACGTCGCGCAGAGCTGGGGA 360  
QY 361 ATGGCCCGCGAGCCAGGCGCGCTTCTCTCTGATGCTTTTGCAGACCGGCTCTG 420  
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QY 541 TCAACCCCTATCGCAAGCCCTCTCCCTACTTTTCTGCGTCCAGACCCCTGAGGAGTGC 600  
Db 541 TCAACCCCTATCGCAAGCCCTCTCCCTACTTTTCTGCGTCCAGACCCCTGAGGAGTGC 600  
QY 601 CTACCACTGAATGAGATAGGGTCCCTTGGCCCCAGGACCTGCCCCCTCCCGGCTGT 660  
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Db 661 CCGGCTCTGGGAGTGACTTTTGAACCGCCACTCCCTTCCCCCACTAGAACTGCTTT 720  
QY 721 TAAATAAATCTCGTAGTTCTCTCAGCTGAGCTAAGCTGGGGCTCTCTTGAACCTGG 780



|||||  
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QY AAGTTCTTCCCTGAGTGTCTCCGAGAGAGGCTGAGCAAAACCACAGCAGGATCCGACGG 900  
Db AAGTTCTTCCCTGAGTGTCTCCGAGAGAGGCTGAGCAAAACCACAGCAGGATCCGACGG 900  
QY GGTTTCCACCTCAGAAAGAAATCGTTTGGCGGTGGGGCGCAAAAGAGTGGGTTGGGA 960  
Db GGTTTCCACCTCAGAAAGAAATCGTTTGGCGGTGGGGCGCAAAAGAGTGGGTTGGGA 960  
QY TCTGAATTTCTTCCACCATTTCCACCCATTTTGGTGAGACTGGGGTGGAGGTCCTAGGGT 1020  
Db TCTGAATTTCTTCCACCATTTCCACCCATTTTGGTGAGACTGGGGTGGAGGTCCTAGGGT 1020  
QY GGGAGGCTCCTGAGAGAGGCTTACCTCGGGGCTTTCCCACTCTTTGGCAATTTGTTCTTTT 1080  
Db GGGAGGCTCCTGAGAGAGGCTTACCTCGGGGCTTTCCCACTCTTTGGCAATTTGTTCTTTT 1080  
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QY 2881 TGACTTTGTTCTTTTATTTTAAATTTTATTTGGCTGAGCAGTGGGGTAAATTTGGCAATGCCAT 2940  
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2941 TTCTGAGATGGTGAAGCCAGAGGAAAGAGCAGTTTGGGGTAAATCAAGGATCTGCAATTTG 3000  
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3961 AGGGTGGGATCACTGTTCACTGTTGACTTCTGGACTATATGGAATAATCAACACAG 4020  
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RESULT 9  
ADG87338  
ID ADG87338 standard; DNA; 10824 BP.  
XX

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4201 TGGTTCAGTTAAACAGGCTGGGATTTTCCAGAGTCCCAACACCTTCAGGTCATCTCTG 4260  
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4741 GTGCTATGGCCCTTGTCTTTTATTAACCAATAATCTTTTGTATATTTATACCTGTATAA 4800  
4801 AAATTTAGAAATGTCAGGCCGGGCAAGTGGCTCACCCCTGTAATCCAGCAGCTTTGGG 4860  
4801 AAATTTAGAAATGTCAGGCCGGGCAAGTGGCTCACCCCTGTAATCCAGCAGCTTTGGG 4860  
4861 AGGCCAGCGGGTGGTCAAGGTCAGGAGTTTTCAGAGCCAGCCTGACCAACATGGTGAA 4920  
4861 AGGCCAGCGGGTGGTCAAGGTCAGGAGTTTTCAGAGCCAGCCTGACCAACATGGTGAA 4920  
4921 ACCCGTCTCTAAAAAATACAAAAATTAGTGGTCAAGTATGCGCAGCTGTAGTCCCA 4980  
4921 ACCCGTCTCTAAAAAATACAAAAATTAGTGGTCAAGTATGCGCAGCTGTAGTCCCA 4980  
4981 GCTAATTTGGAAGGCTGAGGC 5000  
4981 GCTAATTTGGAAGGCTGAGGC 5000



AC ADG87338;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Hereditary haemochromatosis (HH) 24d7 mutant genomic DNA.  
XX  
XX Hereditary haemochromatosis; HH; inherited disorder; iron metabolism;  
KW cirrhosis; diabetes; illness; gene therapy; hepatotropic; mutant; gene;  
KW ds.  
XX  
OS Unidentified.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 361..7147  
FT /\*tag= b  
FT /product= "Hereditary haemochromatosis 24d7 mutant  
FT protein"  
FT exon 361..436  
FT /\*tag= a  
FT intron 437..3761  
FT /\*tag= c  
FT exon 3762..4025  
FT /\*tag= d  
FT intron 4026..4234  
FT /\*tag= e  
FT exon 4235..4510  
FT /\*tag= f  
FT intron 4511..5605  
FT /\*tag= g  
FT exon 5606..5881  
FT /\*tag= h  
FT intron 5882..6038  
FT /\*tag= i  
FT exon 6039..6153  
FT /\*tag= j  
FT intron 6154..7106  
FT /\*tag= k  
FT exon 7107..7147  
FT /\*tag= l  
XX  
PN US2003148972-A1.  
XX  
XX 07-AUG-2003.  
XX  
XX 02-MAY-2002; 2002US-00138888.  
XX  
XX 04-APR-1996; 96US-00630912.  
PR 16-APR-1996; 96US-00632673.  
PR 23-MAY-1996; 96US-00652265.  
PR 04-APR-1997; 97US-00834497.  
PR 04-FEB-2000; 2000US-00497957.  
XX  
PA (BIRA ) BIO-RAD LAB INC.  
XX  
XX Thomas WJ, Drayna DT, Feder JN, Gnrke A, Ruddy D, Tsuchihashi Z;  
PI Wolff RK;  
XX  
XX WPI; 2003-897595/82.  
DR P-PSDB; ADG87337.  
XX  
XX New hereditary hemochromatosis (HH) nucleic acids and peptides, useful  
PT for treating HH leading to diabetes, cirrhosis, sterility or other  
PT serious illnesses.  
XX  
XX Disclosure; SEQ ID NO 79; 122pb; English.  
PS  
XX  
CC The present invention relates to gene and mutations thereto, that are  
CC responsible for the disease hereditary haemochromatosis (HH). Sequences  
CC of the invention are useful for treating hereditary haemochromatosis  
CC which is an inherited disorder or iron metabolism where the body  
CC accumulates excess iron. The excess in iron leads to cirrhosis, diabetes,  
CC and other serious illnesses. The invention is also useful in gene  
CC therapy. The present sequence is hereditary haemochromatosis 24d7 mutant

CC genomic DNA.  
XX  
SQ Sequence 10824 BP; 2996 A; 2253 C; 2646 G; 2929 T; 0 U; 0 Other;  
Query Match 99.9%; Score 4995.2; DB 10; Length 10824;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 4997; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 TCTAAGGTGAGATAAAATTTTAAATGTATGATGATTTTGAATAATTTTGAATAATTTTGA 60  
DB 1 TCTAAGGTGAGATAAAATTTTAAATGTATGATGATTTTGAATAATTTTGAATAATTTTGA 60  
QY 61 AATATCTAAAGTTCAGATCAGAACATTGCGAAGCTACTTTCCCAATCAACACACCCCT 120  
DB 61 AATATCTAAAGTTCAGATCAGAACATTGCGAAGCTACTTTCCCAATCAACACACCCCT 120  
QY 121 TCAGGATTTAAAAACCAAGGGGACACCTGGATCACCTAGTGTCTTTCACAAGCAGGTACCTT 180  
DB 121 TCAGGATTTAAAAACCAAGGGGACACCTGGATCACCTAGTGTCTTTCACAAGCAGGTACCTT 180  
QY 181 CTGCTGTAGGAGAGAGAGAACTAAAGTTCTGAAGACCTGTGTCTTTTTCACAGGAAGTT 240  
DB 181 CTGCTGTAGGAGAGAGAGAACTAAAGTTCTGAAGACCTGTGTCTTTTTCACAGGAAGTT 240  
QY 241 TTACTGGGCATCTCTGAGCCTAGGCAATAGCTGTAGGGTGACCTCTGGAGCCTATCCCG 300  
DB 241 TTACTGGGCATCTCTGAGCCTAGGCAATAGCTGTAGGGTGACCTCTGGAGCCTATCCCG 300  
QY 301 TTTCCTCCGCCCCCAAGAGCGAGATTAAACGGGACGCTGGGGCCAGAGCTGGGGAA 360  
DB 301 TTTCCTCCGCCCCCAAGAGCGAGATTAAACGGGACGCTGGGGCCAGAGCTGGGGAA 360  
QY 361 ATGGCCCGCAGAGCCAGCCCGCGCTTCTCTCTGATGCTTTTTCAGACCGCGTCTCTG 420  
DB 361 ATGGCCCGCAGAGCCAGCCCGCGCTTCTCTCTGATGCTTTTTCAGACCGCGTCTCTG 420  
QY 421 CAGGGCGCTTGTGCGTGTGCTGAGTCCGAGGGTCCGGGGAACTAGGGGGCGCGGGGTG 480  
DB 421 CAGGGCGCTTGTGCGTGTGCTGAGTCCGAGGGTCCGGGGAACTAGGGGGCGCGGGGTG 480  
QY 481 GAAAAATCGAAACTAGCTTTTCTTTGCGCTTGGGAGTTTGTAACTTTGAGAGCACTGC 540  
DB 481 GAAAAATCGAAACTAGCTTTTCTTTGCGCTTGGGAGTTTGTAACTTTGAGAGCACTGC 540  
QY 541 TCAACCTATCCGCAAGCCCTCTCCCTACTCTTCTGCTCCAGACCCCGTGGAGAGTGC 600  
DB 541 TCAACCTATCCGCAAGCCCTCTCCCTACTCTTCTGCTCCAGACCCCGTGGAGAGTGC 600  
QY 601 CTACCACTGAAGTGCAGATAGGGTCCCTCGCCCGCAGGACCTGCCCTCCCGGCTGT 660  
DB 601 CTACCACTGAAGTGCAGATAGGGTCCCTCGCCCGCAGGACCTGCCCTCCCGGCTGT 660  
QY 661 CCCGCTCTGCGAGTGACTTTTGGAAACCGCCCACTCCCTTTCCCCCAACTAGAATGCTTT 720  
DB 661 CCCGCTCTGCGAGTGACTTTTGGAAACCGCCCACTCCCTTTCCCCCAACTAGAATGCTTT 720  
QY 721 TAAATAAATCTCGTAGTTCTCTCACTTGAGCTGAGCTAAGCTGGGCTCTTGAACCTGG 780  
DB 721 TAAATAAATCTCGTAGTTCTCTCACTTGAGCTGAGCTAAGCTGGGCTCTTGAACCTGG 780  
QY 781 AACTCGGGTTATTTTCCAATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 840  
DB 781 AACTCGGGTTATTTTCCAATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 840  
QY 841 AAGTTCTTCCCTGAGTGTGCTTCCGAGAGGCTGAGCAAAACCCACAGCAGGATCCGACGG 900  
DB 841 AAGTTCTTCCCTGAGTGTGCTTCCGAGAGGCTGAGCAAAACCCACAGCAGGATCCGACGG 900  
QY 901 GGTTCACCTCAGAACGAATCGTGGCGGTGGGGCGGGAAGAGTGGGTGGGA 960  
DB 901 GGTTCACCTCAGAACGAATCGTGGCGGTGGGGCGGGAAGAGTGGGTGGGA 960  
QY 961 TCTGAATTTCTTCCACCATTTCCACCCCACTTTTGGTGTGAGACCTGGGGTGGAGGTCTCTAGGGT 1020



Db 961 |||||TCTGAAATTTCTACCAATTCACCCACATTTTGGTGAGACCTGGGGTCTCTAGGGT 1020  
Qy 1021 GGGAGGCTCTGAGAGAGGCTTACCTCGGGCCCTTTCCCACTCTCTGGCAATTCCTTTT 1080  
Db 1021 GGGAGGCTCTGAGAGAGGCTTACCTCGGGCCCTTTCCCACTCTCTGGCAATTCCTTTT 1080  
Qy 1081 GCCTGGAAATTAAGTATATGTTAGTTTGAACGTTTGAACCTGAACAAATTCCTTTTCGG 1140  
Db 1081 GCCTGGAAATTAAGTATATGTTAGTTTGAACGTTTGAACCTGAACAAATTCCTTTTCGG 1140  
Qy 1141 CTAGGCTTTATTCATTTGCAATGCTGTGTAAATTAAGAGGCTCTCTCAAAAGTACTGA 1200  
Db 1141 CTAGGCTTTATTCATTTGCAATGCTGTGTAAATTAAGAGGCTCTCTCAAAAGTACTGA 1200  
Qy 1201 TAATGAACATGTAAGCAATGCACTCACTTCTTAAGTTTACATTTCAATCTGATCTTATTTGA 1260  
Db 1201 TAATGAACATGTAAGCAATGCACTCACTTCTTAAGTTTACATTTCAATCTGATCTTATTTGA 1260  
Qy 1261 TTTTCACTAGGCATAGGGAGGTAGGAGCTAATAATACGTTTATTTTACTAGAAGTTAACT 1320  
Db 1261 TTTTCACTAGGCATAGGGAGGTAGGAGCTAATAATACGTTTATTTTACTAGAAGTTAACT 1320  
Qy 1321 GGAATTCAGATTAATACTCTTTTCAGTTTCAAAAGAACATAAATACTGTTTCTG 1380  
Db 1321 GGAATTCAGATTAATACTCTTTTCAGTTTCAAAAGAACATAAATACTGTTTCTG 1380  
Qy 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTGACAGTGAATTTTGGCCCTG 1440  
Db 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTGACAGTGAATTTTGGCCCTG 1440  
Qy 1441 TGTAGCACAGTGTCTGTGGGTCAACGCGGCTCAGCACAGCACTTTGAGTTTGGTA 1500  
Db 1441 TGTAGCACAGTGTCTGTGGGTCAACGCGGCTCAGCACAGCACTTTGAGTTTGGTA 1500  
Qy 1501 CTACGTGTATCCATTTTACATGACAGAAATAGGCAAGGCAAGGCTGCTTCTG 1560  
Db 1501 CTACGTGTATCCATTTTACATGACAGAAATAGGCAAGGCAAGGCTGCTTCTG 1560  
Qy 1561 CAAATTTATTTCAATGTACACTGGGCTTTGGTGGCAGAGCTCATGCTCCACTTCATAGC 1620  
Db 1561 CAAATTTATTTCAATGTACACTGGGCTTTGGTGGCAGAGCTCATGCTCCACTTCATAGC 1620  
Qy 1621 TATGATTTCTTAAACATCACACTGCAATTAGAGTTGAATAATAAATTTTCAATGTAGCAG 1680  
Db 1621 TATGATTTCTTAAACATCACACTGCAATTAGAGTTGAATAATAAATTTTCAATGTAGCAG 1680  
Qy 1681 AAATATTCATTTGTTTAAAGTAAATAGTCCAGCCATGTGTGCACTGTTCAAGCCC 1740  
Db 1681 AAATATTCATTTGTTTAAAGTAAATAGTCCCTTCCATGTGTTGCACTGTTCAAGCCC 1740  
Qy 1741 CAAGGAGAGACAGGGAACAGTCTTTTACCCTTTGATATTTTGCATTTCTAGTGGAGA 1800  
Db 1741 CAAGGAGAGACAGGGAACAGTCTTTTACCCTTTGATATTTTGCATTTCTAGTGGAGA 1800  
Qy 1801 GATGACAAATAGCAATGAGCAGAAAGATATACACATCAGGAAATCATGGGTGTTGTGA 1860  
Db 1801 GATGACAAATAGCAATGAGCAGAAAGATATACACATCAGGAAATCATGGGTGTTGTGA 1860  
Qy 1861 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGCTGACACTTGAGCAGACATGAAGGA 1920  
Db 1861 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGCTGACACTTGAGCAGACATGAAGGA 1920  
Qy 1921 AATAAGAAATGATATTTCACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAAG 1980  
Db 1921 AATAAGAAATGATATTTCACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAAG 1980  
Qy 1981 TTGGATTTAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040  
Db 1981 TTGGATTTAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040  
Qy 2041 CGGCGTGGGGTGGGAAGGGGAGCTACCATCTGCATGTAGGATGCTTAGCAGTATCCTGT 2100  
Db |||||

Db 2041 CGGCGTGGGGTGGGAAGGGGAGCTACCATCTGCATGTAGGATGCTTAGCAGTATCCTGT 2100  
Qy 2101 CTTCCCTACTCTACTAGTGTCTAGGAGCACTCCCCAGTCTTGACAAACAAAAATGCTCT 2160  
Db 2101 CTTCCCTACTCTACTAGTGTCTAGGAGCACTCCCCAGTCTTGACAAACAAAAATGCTCT 2160  
Qy 2161 AAATCTTGGCCACATGTCACCTAGTAGACAAATCTCTGGTTTAAAGAGCTCGGGTTGAAA 2220  
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Db 2221 AATAAACAGTATGCTCTGGGAGTAGAGGCCAAGAAGTAGGTAATGGGCTCAGAAAGGA 2280  
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Db 2281 GCCACAAACAAAGTGTGAGCGCTGTAGGCTGTGGTGTGAATTTCTAGCCAAAGAGTA 2340  
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Db 2341 ACAGTGATCTGTACAGGGCTTTTAAAGATTGCTCTGGCTGTATGTGAAAGCAGAAATG 2400  
Qy 2401 AAGGAGCAACAGTAAAGCAGGAGCCAGCCAGGAGAGCTTTACACAGTCCAGCAAG 2460  
Db 2401 AAGGAGCAACAGTAAAGCAGGAGCCAGCCAGGAGAGCTTTACACAGTCCAGCAAG 2460  
Qy 2461 AGGTAGTGGAGTGGGCTGGGTCGGAACAGAAAGGAGTGACAAACATTTGCTCTGAA 2520  
Db 2461 AGGTAGTGGAGTGGGCTGGGTCGGAACAGAAAGGAGTGACAAACATTTGCTCTGAA 2520  
Qy 2521 TATATTTGAAAGAAAGTTGCTGAAGGATTTCTATGTTGTGTGAGAGAAAGAGAAATGG 2580  
Db 2521 TATATTTGAAAGAAAGTTGCTGAAGGATTTCTATGTTGTGTGAGAGAAAGAGAAATGG 2580  
Qy 2581 CTGGGTGTAGTGTCTATGCCAAGAGAGAGGCCAAGAGAGAGAGATTTCTGTAGCTCAGGA 2640  
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Qy 2641 GTTCAAGACACGCTGGGCAACACAGCAAAACCCCTTCTACAAAAATACAAAAATTA 2700  
Db 2641 GTTCAAGACACGCTGGGCAACACAGCAAAACCCCTTCTACAAAAATACAAAAATTA 2700  
Qy 2701 GCTGGGTGTGGTGGCATGCCTGTGATCTTAGCTACTCGGGAGGCTGAGGTGGAGGTA 2760  
Db 2701 GCTGGGTGTGGTGGCATGCACCTGTGATCTTAGCTACTCGGGAGGCTGAGGTGGAGGTA 2760  
Qy 2761 TTGCTTGAGCCAGAGAGTTGAGGCTGCAGTGAGGCAATGACTGTGCTTCTTACCTCAGC 2820  
Db 2761 TTGCTTGAGCCAGAGAGTTGAGGCTGCAGTGAGGCAATGACTGTGCTTCTTACCTCAGC 2820  
Qy 2821 CTAGGTGACAGAGCAAGACCCCTGCTCCCTGACCCCTGAAAAAGAGAGAGTTAAAGT 2880  
Db 2821 CTAGGTGACAGAGCAAGACCCCTGCTCCCTGACCCCTGAAAAAGAGAGAGTTAAAGT 2880  
Qy 2881 TGACTTTGTTCTTTTATTTTAAATTTTATTTGGCTGTAGCAGTGGGTAAATTTGGCAATGCCAT 2940  
Db 2881 TGACTTTGTTCTTTTATTTTAAATTTTATTTGGCTGTAGCAGTGGGTAAATTTGGCAATGCCAT 2940  
Qy 2941 TTCTGAGATGTTGAAGGAGAGAGAGAGAGAGTGGGTAAATCAAGGATCTGCATTTG 3000  
Db 2941 TTCTGAGATGTTGAAGGAGAGAGAGAGAGAGTGGGTAAATCAAGGATCTGCATTTG 3000  
Qy 3001 GGACATGTTAAGTTTGAATTTCCAGTCTAGGCTTTCCAGTGGGTGAGGCCACATAGGCAGTT 3060  
Db 3001 GGACATGTTAAGTTTGAATTTCCAGTCTAGGCTTTCCAGTGGGTGAGGCCACATAGGCAGTT 3060  
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Db 3061 CAGTGTAAAGAAATTCAGGACCAAGGCTGGGCAAGGCTGCTCTCTGTAAATCCCAGCACT 3120  
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Db 3121 TTGGTGGCTGAGGCAAGGTAGATCAATTTGAGGTCAGAGTTTGAGACAAGCTTTGGCCAAACA 3180















3061 QY CAGTGTAAAGATTTCAGACCAAGGCTGGGCA CGGTGGCTCACTTCTGTAAATCCAGCACT 3120  
3061 Db CAGTGTAAAGATTTCAGACCAAGGCTGGGCA CGGTGGCTCACTTCTGTAAATCCAGCACT 3120  
3121 QY TTGGTGGCTGAGCAGGTAGATCATTTTGGGTGAGGTGAGAGTTTGAGACAAGCTTTGGCCAAACA 3180  
3121 Db TTGGTGGCTGAGCAGGTAGATCATTTTGGGTGAGGTGAGAGTTTGAGACAAGCTTTGGCCAAACA 3180  
3181 QY TGGTGAACCCCAATGCTTACTTAAATAACAAAAATAGCTGGTGGTGGGCGACCGCT 3240  
3181 Db TGGTGAACCCCAATGCTTACTTAAATAACAAAAATAGCTGGTGGTGGGCGACCGCT 3240  
3241 QY ATAGTCCCAAGTTTTCAGAGGCTTAGGTAGGAGAAATCCCTTGAACCCAGGAGGTGCAGG 3300  
3241 Db ATAGTCCCAAGTTTTCAGAGGCTTAGGTAGGAGAAATCCCTTGAACCCAGGAGGTGCAGG 3300  
3301 QY TTGCAGTGAGCTGAGATTTGGCCACTGCACTCAGGCTGGGTGATAGATGAGACTCTGT 3360  
3301 Db TTGCAGTGAGCTGAGATTTGGCCACTGCACTCAGGCTGGGTGATAGATGAGACTCTGT 3360  
3361 QY CTCAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 3420  
3361 Db CTCAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 3420  
3421 QY TCTAATTTGCCCTGAGCA CCAACTCTCTGAGTTCAACTACCATGCTGCTAGACACACCTTTAAC 3480  
3421 Db TCTAATTTGCCCTGAGCA CCAACTCTCTGAGTTCAACTACCATGCTGCTAGACACACCTTTAAC 3480  
3481 QY ATTTTCTAGAAATCCACAGCTTTAGTGGAGTCTGTCTAATCATGATATTTGAATAGGAT 3540  
3481 Db ATTTTCTAGAAATCCACAGCTTTAGTGGAGTCTGTCTAATCATGATATTTGAATAGGAT 3540  
3541 QY CTGGGGGAGTGGAGGGTGGCAGCCAGCTGTGGCAGAGAAAGACACACAAGGAAAGAGC 3600  
3541 Db CTGGGGGAGTGGAGGGTGGCAGCCAGCTGTGGCAGAGAAAGACACACAAGGAAAGAGC 3600  
3601 QY ACCCAGGACTGTATATGGAAGAAAGACAGGAGCTGCAACTACCCCTTCAAAAAATGAGGA 3660  
3601 Db ACCCAGGACTGTATATGGAAGAAAGACAGGAGCTGCAACTACCCCTTCAAAAAATGAGGA 3660  
3661 QY CCAGACAGAGCTGATGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3720  
3661 Db CCAGACAGAGCTGATGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3720  
3721 QY CTCCTACTACATGTTTAAAGCTGTTCTCTCTCTCCAGGTTCACACTCTCTGACATA 3780  
3721 Db CTCCTACTACATGTTTAAAGCTGTTCTCTCTCTCCAGGTTCACACTCTCTGACATA 3780  
3781 QY CCTCTTTCATGGGTGCTCAGACAGGACCTTGGTCTTTCTTTTGAAGCTTTGGGCTA 3840  
3781 Db CCTCTTTCATGGGTGCTCAGACAGGACCTTGGTCTTTCTTTTGAAGCTTTGGGCTA 3840  
3841 QY CGTGGATGACAGCTGTTCTGTTCTATGATCATGAGAGTCCGCTGTGGAGCCCGGAAAC 3900  
3841 Db CGTGGATGACAGCTGTTCTGTTCTATGATCATGAGAGTCCGCTGTGGAGCCCGGAAAC 3900  
3901 QY TCCATGGGTTTCCAGTGAAGTTTCAAGCCAGATGTGGCTGACAGTGCAGAGTCTGAA 3960  
3901 Db TCCATGGGTTTCCAGTGAAGTTTCAAGCCAGATGTGGCTGACAGTGCAGAGTCTGAA 3960  
3961 QY AGGGTGGGATCATGTTTCACTGTTGACTTTCTGGACTATTATGGAATAATCAACACACAG 4020  
3961 Db AGGGTGGGATCATGTTTCACTGTTGACTTTCTGGACTATTATGGAATAATCAACACACAG 4020  
4021 QY CAAGGGTATGTGGAGAGGGGGCTCACCTTCTGAGGTTGTGAGAGCTTTTCACTTTTC 4080  
4021 Db CAAGGGTATGTGGAGAGGGGGCTCACCTTCTGAGGTTGTGAGAGCTTTTCACTTTTC 4080  
4081 QY ATGCAATCTTGAAGAAACAGCTGGAAGTCTGAGTCTGAGTGGAGCAGGAGAGGAG 4140  
4081 Db ATGCAATCTTGAAGAAACAGCTGGAAGTCTGAGTCTGAGTGGAGCAGGAGAGGAG 4140  
4141 QY GAAATTTGCTTCTGAGATCATTTTGGTCTTGGGATGTTGGAAATAGGACCTATTCTT 4200

4141 Db GAAATTTGCTTCTGAGATCATTTTGGTCTTGGGATGTTGGAAATAGGACCTATTCTT 4200  
4201 QY TGGTTGCAAGTTTAAACAAGGCTGGGATTTTCCAGAGTCCCA CACCTTGAGTCACTCTG 4260  
4201 Db TGGTTGCAAGTTTAAACAAGGCTGGGATTTTCCAGAGTCCCA CACCTTGAGTCACTCTG 4260  
4261 QY GGCTGTGAAATCAAGAAGACAAAGTACCGAGGGCTACTCGGAAGTACCGGTATGATGG 4320  
4261 Db GGCTGTGAAATCAAGAAGACAAAGTACCGAGGGCTACTCGGAAGTACCGGTATGATGG 4320  
4321 QY CAGGACCACTTTGAATTTGCTGCTGACACACTTGGATTTGAGAGCAGACAGAACCCAGGGCC 4380  
4321 Db CAGGACCACTTTGAATTTGCTGCTGACACACTTGGATTTGAGAGCAGACAGAACCCAGGGCC 4380  
4381 QY TGGCCCAACCAAGCTGGAGTGGGAAAGGACAAAGATTCGGGCCAGGACAGAGGCTTAC 4440  
4381 Db TGGCCCAACCAAGCTGGAGTGGGAAAGGACAAAGATTCGGGCCAGGACAGAGGCTTAC 4440  
4441 QY CTGGAGAGGGACTGCTGCTGACAGCTGACAGAGTGTCTGAGCTGGGAGAGGTGTTTG 4500  
4441 Db CTGGAGAGGGACTGCTGCTGACAGCTGACAGAGTGTCTGAGCTGGGAGAGGTGTTTG 4500  
4501 QY GACCAACAAGGTATGGTGGAAACA CACTTCTGCCCTATPACTCTAGTGGCAGAGTGGAG 4560  
4501 Db GACCAACAAGGTATGGTGGAAACA CACTTCTGCCCTATPACTCTAGTGGCAGAGTGGAG 4560  
4561 QY AGGTTGCAAGGACCAAGGATCCCTGTTGGAGTTTCAGAGTGGCTGAGGCTGTGCTC 4620  
4561 Db AGGTTGCAAGGACCAAGGATCCCTGTTGGAGTTTCAGAGTGGCTGAGGCTGTGCTC 4620  
4621 QY TCCAAATTTCTGGGAAAGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTTGAGATGTA 4680  
4621 Db TCCAAATTTCTGGGAAAGGACTTTCTCAATCCTAGAGTCTCTACCTTATAATTTGAGATGTA 4680  
4681 QY TGAGACAGCCCAAGTCAATGAGTTTAAATTTCTTCTCCATGCATATGGCTCAAGGGAA 4740  
4681 Db TGAGACAGCCCAAGTCAATGAGTTTAAATTTCTTCTCCATGCATATGGCTCAAGGGAA 4740  
4741 QY GTGCTATGAGGCTTGTCTTTTATTTAAACCAATATCTTTTGTATATTTATACCTGTTAA 4800  
4741 Db GTGCTATGAGGCTTGTCTTTTATTTAAACCAATATCTTTTGTATATTTATACCTGTTAA 4800  
4801 QY AAATTCAGAAATGTCAAGCCGGGCA CGGTGGCTCACCCCTGTAATCCAGCACTTTGG 4860  
4801 Db AAATTCAGAAATGTCAAGCCGGGCA CGGTGGCTCACCCCTGTAATCCAGCACTTTGG 4860  
4861 QY AGGCCGAGCGGGTGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAG 4920  
4861 Db AGGCCGAGCGGGTGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAG 4920  
4921 QY ACCCGTCTCTAAAAAATAACAAAAATAGCTGGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 4980  
4921 Db ACCCGTCTCTCTAAAAAATAACAAAAATAGCTGGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 4980  
4981 QY GCTAATTTGAAAGGCTGAGGC 5000  
4981 Db GCTAATTTGAAAGGCTGAGGC 5000

## RESULT 11

AAV57926/c

ID AAV57926 standard; DNA; 235033 BP.

XX AAV57926;

AC AAV57926;

XX 23-DEC-1998 (first entry)

XX Hereditary haemochromatosis subregion from an unaffected individual.

DE Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE;

XX diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3; BTF4;

KW BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;

KW BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;



KW type 1 sodium transport gene; ss.  
XX Homo sapiens.  
OS WO9814466-A1.  
PN 09-APR-1998.  
XX 30-SEP-1997; 97WO-US017658.  
XX 01-OCT-1996; 96US-00724394.  
PR 07-MAY-1997; 97US-00852495.  
XX (PROG-) PROGENITOR INC.  
XX Feder JN, Kronmal GS, Lauer PM, Ruddy DA, Thomas WJ;  
PI Tsuchihashi Z, Wolff RK;  
XX WPI; 1998-240014/21.  
XX Hereditary haemochromatosis gene products - used to develop products for  
PT the diagnosis and treatment of hereditary disorders in iron metabolism.  
XX Example 2; Fig 8; 209pp; English.  
XX The present invention describes hereditary haemochromatosis gene products  
CC from the human haemochromatosis gene. The present sequence represents a  
CC hereditary haemochromatosis subregion from an individual unaffected by  
CC hereditary haemochromatosis (HH). Also described is a method to determine  
CC the presence or absence of the common hereditary haemochromatosis (HFE)  
CC gene mutation in an individual comprising: (a) providing DNA or RNA from  
CC the individual; and (b) assessing the DNA or RNA for the presence or  
CC absence of a haplotype or genotype where the presence or absence of the  
CC haplotype genotype indicates the likely presence of the HFE gene mutation  
CC in the genome of the individual. The HFE gene sequences from the present  
CC invention can be used to develop products for use in the diagnosis and  
CC treatment of HFE. The present invention also describes BTF genes, which  
CC are homologues of the milk protein butyrophilin (BT), and can be used in  
CC the production of agonists and antagonists of BT function. Also described  
CC are: (1) a RoRet gene which can be used to develop products for the  
CC study, diagnosis and treatment of lupus and Sjogren's syndrome; and (2)  
CC NPT3 and NPT4 genes which are homologues of a type 1 sodium transport  
CC gene, and can similarly be used for hypophosphatemia  
XX  
SQ Sequence 235033 BP; 68786 A; 48466 C; 49441 G; 68340 T; 0 U; 0 Other;  
Query Match 99.8%; Score 4988; DB 2; Length 235033;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4999; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 TCTAAGGTGAGATAAAATTTTAAATGATGATGAAATTTTGAATAATCATAAATATTTA 47089  
DB 47148 TCTAAGGTGAGATAAAATTTTAAATGATGATGAAATTTTGAATAATCATAAATATTTA 47089  
QY 61 AATATCTAAAGTTTCAGATCAGAACATTCGAGAGTACTTTCCCAATCAACAAACCCCT 120  
DB 47088 AATACTAAAGTTTCAGATCAGAACATTCGAGAGTACTTTCCCAATCAACAAACCCCT 47029  
QY 121 TCAGAGTTTAAACCAAGGGGGACACTGGATCACCTAGTGTGTTTCAACAGCAGGTACCTT 180  
DB 47028 TCAGAGTTTAAACCAAGGGGGACACTGGATCACCTAGTGTGTTTCAACAGCAGGTACCTT 46969  
QY 181 CTGCTGTAGGAGAGAGAGACTAAAGTTCTGAAGACCTGTGCTTTTCAACAGAGAGTTT 240  
DB 46968 CTGCTGTAGGAGAGAGAGACTAAAGTTCTGAAGACCTGTGCTTTTCAACAGAGAGTTT 46909  
QY 241 TTACTGGGCACTCTCTGAGCCCTAGCAATAGCTGTAGGTGACTTCTTGAGCCATCCCG 300  
DB 46908 TTACTGGGCACTCTCTGAGCCCTAGCAATAGCTGTAGGTGACTTCTTGAGCCATCCCG 46849  
QY 301 TTTCCCGCCCCCAAAAGACGGAGATTTTAAACGGGACGTCGGCCAGAGCTCGGAA 360  
DB 46848 TTTCCCGCCCCCAAAAGACGGAGATTTTAAACGGGACGTCGGCCAGAGCTCGGAA 46789

QY 361 ATGGCCCGCGAGCCAGCCAGCCGCGCTTCTCTCTGATGCTTTTGCAGACGCGGTCTCTG 420  
DB 46788 ATGGCCCGCGAGCCAGCCAGCCGCGCTTCTCTCTGATGCTTTTGCAGACGCGGTCTCTG 46729  
QY 421 CAGGGGCGCTTGTGCTGCTGAGTCCGAGGGCTGCGGGCGAACTAGGGGCGCGCGGGGTG 480  
DB 46728 CAGGGGCGCTTGTGCTGCTGAGTCCGAGGGCTGCGGGCGAACTAGGGGCGCGCGGGGTG 46669  
QY 481 GAAAAATCGAAAACTAGCTTTTTTCTTTGCGCTTGGGAGTTTGTCTAACTTTGAGGACCTGTC 540  
DB 46668 GAAAAATCGAAAACTAGCTTTTTTCTTTGCGCTTGGGAGTTTGTCTAACTTTGAGGACCTGTC 46609  
QY 541 TCAACCTTATCGCAAGCCCTCTCCCTACTCTTTCTGCGTCCAGACCCCGTGAAGGAGTGC 600  
DB 46608 TCAACCTTATCGCAAGCCCTCTCCCTACTCTTTCTGCGTCCAGACCCCGTGAAGGAGTGC 46549  
QY 601 CTACCACTGAATGCGAGATAGGGGTCCCTCCGCCAGGACCTGCCCCCTCCCCGGCTGT 660  
DB 46548 CTACCACTGAATGCGAGATAGGGGTCCCTCCGCCAGGACCTGCCCCCTCCCCGGCTGT 46489  
QY 661 CCGGCTCTCGGGAGTGAATTTTGGAAACCGCCACTCCCTTCCGCCAACTAGAAATGCTTT 720  
DB 46488 CCGGCTCTCGGGAGTGAATTTTGGAAACCGCCACTCCCTTCCGCCAACTAGAAATGCTTT 46429  
QY 721 TAAATAATCTCGTAGTTCTCTCACTTGAGCTGAGCTAAGCCTGGGCTCCTTGACCTGG 780  
DB 46428 TAAATAATCTCGTAGTTCTCTCACTTGAGCTGAGCTAAGCCTGGGCTCCTTGACCTGG 46369  
QY 781 AACTCGGGTGTATTTTCCAATGTGAGCTGTGAGTTTTTTTCCCGAGTCACTATCCAAACAGG 840  
DB 46368 AACTCGGGTGTATTTTCCAATGTGAGCTGTGAGTTTTTTTCCCGAGTCACTATCCAAACAGG 46309  
QY 841 AAGTTTCTCTGAGTGTCTTCCGAGAAAGCTGAGCAAAACCCACAGAGGATCCGACGG 900  
DB 46308 AAGTTTCTCTGAGTGTCTTCCGAGAAAGCTGAGCAAAACCCACAGAGGATCCGACGG 46249  
QY 901 GGTTCACCTCAGAACGAATCGTGGCGGTGGGGCGGGAAGAGCTGGGTTGGGA 960  
DB 46248 GGTTCACCTCAGAACGAATCGTGGCGGTGGGGCGGGAAGAGCTGGGTTGGGA 46189  
QY 961 TCTGAATTTCTTCAACCATTTCCACCCACTTTTGGTGAGACTCTGGGTGAGGCTCTAGGGT 1020  
DB 46188 TCTGAATTTCTTCAACCATTTCCACCCACTTTTGGTGAGACTCTGGGTGAGGCTCTAGGGT 46129  
QY 1021 GGGAGGCTCTTGAGAGAGGCTTACCTCGGGCTTTTCCCACTCTTTGGCAAATGTTCTTTT 1080  
DB 46128 GGGAGGCTCTTGAGAGAGGCTTACCTCGGGCTTTTCCCACTCTTTGGCAAATGTTCTTTT 46069  
QY 1081 GCCTGGAAAAATTAAGTATATGTTTGAACGTTTGAACCTGAACTGAACAATTTCTTTTTCGG 1140  
DB 46068 GCCTGGAAAAATTAAGTATATGTTTGAACGTTTGAACCTGAACTGAACAATTTCTTTTTCGG 46009  
QY 1141 CTAGGCTTTTATGATTTTGCATTTGCTGTGTAATTAAGAGGCTCTCTACAAAGTACTGA 1200  
DB 46008 CTAGGCTTTTATGATTTTGCATTTGCTGTGTAATTAAGAGGCTCTCTACAAAGTACTGA 45949  
QY 1201 TAATGAACATGTAGCAATGCACTCACTTCTAAGTTTCAATTCATTCATTCATTCATTTGA 1260  
DB 45948 TAATGAACATGTAGCAATGCACTCACTTCTAAGTTTCAATTCATTCATTCATTCATTTGA 45889  
QY 1261 TTTTCACTAGGCATAGGGAGGTAGGAGCTAATAATACGTTTATTTTACTAGAAATTAAT 1320  
DB 45888 TTTTCACTAGGCATAGGGAGGTAGGAGCTAATAATACGTTTATTTTACTAGAAATTAAT 45829  
QY 1321 GGAATTCAGATTTATATACTCTTTTTCAGGTTTCAAAAGAACATAAATAATCTGGTTTCTG 1380  
DB 45828 GGAATTCAGATTTATATACTCTTTTTCAGGTTTCAAAAGAACATAAATAATCTGGTTTCTG 45769  
QY 1381 ATGTTTATTTCAAGTACTACAGCTGCTTAATCTTAGTTTGAAGTATTTGCCCCCTGTAG 1440  
DB 45768 ATGTTTATTTCAAGTACTACAGCTGCTTAATCTTAGTTTGAAGTATTTGCCCCCTGTAG 45709



QY	1441	TGTAGCACAGTGTCTCTGTGGGTACACGCGCGCTCAGCACAGCACTTTTGTGGTA	1500
Db	45708	TGTAGCACAGTGTCTCTGTGGGTACACGCGCGCTCAGCACAGCACTTTTGTGGTA	45649
QY	1501	CTACGTGTATCCACATTTTACACATCACAGANTGAGGCATGGCAGGGCTGCTTCTCTGG	1560
Db	45648	CTACGTGTATCCACATTTTACACATCACAGANTGAGGCATGGCAGGGCTGCTTCTCTGG	45589
QY	1561	CAAAATTTATTTCAATGTGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC	1620
Db	45588	CAAAATTTATTTCAATGTGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC	45529
QY	1621	TATGATTTCTTAAACATCACATGTCATTTAGAGTTGAAATATAAATTTTATGTTGAGCAG	1680
Db	45528	TATGATTTCTTAAACATCACATGTCATTTAGAGTTGAAATATAAATTTTATGTTGAGCAG	45469
QY	1681	AAATATTTCAATGTTTACAGTGTAAATGATGCCAGCCATGTTTGCATGTTTCAAGCCC	1740
Db	45468	AAATATTTCAATGTTTACAGTGTAAATGATGCCAGCCATGTTTGCATGTTTCAAGCCC	45409
QY	1741	CAAGGAGAGAGCAGGGAAACAAGTCTTTTACCTTTTGATATTTTGTCAATTTAGTGGGAGA	1800
Db	45408	CAAGGAGAGAGCAGGGAAACAAGTCTTTTACCTTTTGATATTTTGTCAATTTAGTGGGAGA	45349
QY	1801	GATGACAAATAGCAATAGCAGAAAGATATACAAATCAGGAAATCATGGGTGTTGTGA	1860
Db	45348	GATGACAAATAGCAATAGCAGAAAGATATACAAATCAGGAAATCATGGGTGTTGTGA	45289
QY	1861	GAAGCAGAGAGTCAGGCGAAGTCACTCTGGGCTGACACTTGGAGCAGACATGAGGA	1920
Db	45288	GAAGCAGAGAGTCAGGCGAAGTCACTCTGGGCTGACACTTGGAGCAGACATGAGGA	45229
QY	1921	AAATAAGAAATGATATTCACCTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAAG	1980
Db	45228	AAATAAGAAATGATATTCACCTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAAG	45169
QY	1981	TTGGATTTAAAAACGCGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG	2040
Db	45168	TTGGATTTAAAAACGCGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG	45109
QY	2041	CGGCGTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGCTACAGTATCCTGT	2100
Db	45108	CGGCGTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGCTACAGTATCCTGT	45049
QY	2101	CCTCCCTACTCACTAGGTGCTAGGAGCACTCCCCAGTCTTGACAAACAAAAATGCTCT	2160
Db	45048	CCTCCCTACTCACTAGGTGCTAGGAGCACTCCCCAGTCTTGACAAACAAAAATGCTCT	44989
QY	2161	AAACTTTGCCACATGTCACCTAGTAGACAAACTCTGGTTAAGAAAGCTCGGGTTGAAAA	2220
Db	44988	AAACTTTGCCACATGTCACCTAGTAGACAAACTCTGGTTAAGAAAGCTCGGGTTGAAAA	44929
QY	2221	AATAAACAAGTAGTGTCTGGGAGTAGAGGCCAAGAAGTAGGTAAATGGGCTCAGAGAGGA	2280
Db	44928	AATAAACAAGTAGTGTCTGGGAGTAGAGGCCAAGAAGTAGGTAAATGGGCTCAGAGAGGA	44869
QY	2281	GCCACAAAACAAGTGTGAGGCGCTGTAGGCTGTGTGTGAAATTTCTAGCCAAAGAGTA	2340
Db	44868	GCCACAAAACAAGTGTGAGGCGCTGTAGGCTGTGTGTGAAATTTCTAGCCAAAGAGTA	44809
QY	2341	ACAGTGATCTGTACAGGCTTTTAAAGAATGCTCTGGCTGTATGTGGAAAGCAGAAATG	2400
Db	44808	ACAGTGATCTGTACAGGCTTTTAAAGAATGCTCTGGCTGTATGTGGAAAGCAGAAATG	44749
QY	2401	AGGGAGCAACAGTAAAGCAGGGGCCAGCCAGCAAGCACTGTTACAGTCCAGGCAAG	2460
Db	44748	AGGGAGCAACAGTAAAGCAGGGGCCAGCCAGCAAGCACTGTTACAGTCCAGGCAAG	44689
QY	2461	AGGTAGTGGAGTGGGCTGGGTGGAAACAGAAAGGGAGTGACAAACATTTGCTCTGAA	2520
Db	44688	AGGTAGTGGAGTGGGCTGGGTGGAAACAGAAAGGGAGTGACAAACATTTGCTCTGAA	44629
QY	2521	TATATTTCTGAAGGAAGTTGCTGAAGGATTTCTATGTTGTGTGAGAGAAAGAGAATTTGG	2580

Db	44628	TATATTTCTGAAGGAAGTTGCTGAAGGATTTCTATGTTGTGTGAGAGAAAGAGAATTTGG	44569
QY	2581	CTGGGTGTAGTAGTCTATGCCCAAGGAGGAGGCCAAGGAGCAGAGATTTCTTGAGCTCAGGA	2640
Db	44568	CTGGGTGTAGTAGTCTATGCCCAAGGAGGAGGCCAAGGAGCAGAGATTTCTTGAGCTCAGGA	44509
QY	2641	GTTTCAAGACACAGCCTGGGCAACACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA	2700
Db	44508	GTTTCAAGACACAGCCTGGGCAACACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA	44449
QY	2701	GCTGGGTGTGGCATGCCATGCCCTGTGATCTCTAGTCTACTCGGAGGCTGAGGTGGAGGTTA	2760
Db	44448	GCTGGGTGTGGCATGCCATGCCCTGTGATCTCTAGTCTACTCGGAGGCTGAGGTGGAGGTTA	44389
QY	2761	TTGCTTTGAGCCAGGAGTTGAGGCTTGAGTCAGTCAGGCATGCTGTCACCTGTACTTTCCAG	2820
Db	44388	TTGCTTTGAGCCAGGAGTTGAGGCTTGAGTCAGTCAGGCATGCTGTCACCTGTACTTTCCAG	44329
QY	2821	CTAGGTGACAGAGCAAGACCCCTGTCTCCCTGACCCCTGAAAAAGAGAGAGTTTAAAGT	2880
Db	44328	CTAGGTGACAGAGCAAGACCCCTGTCTCCCTGACCCCTGAAAAAGAGAGAGTTTAAAGT	44269
QY	2881	TGACCTTTGTTCTTTATTTTAAATTTTGGCTTGAGCAGTGGGTTAATTTGGCAATGCCAT	2940
Db	44268	TGACCTTTGTTCTTTATTTTAAATTTTGGCTTGAGCAGTGGGTTAATTTGGCAATGCCAT	44209
QY	2941	TTCTCAGATGGTGAAGGAGAGGAAGAGCAGTTTGGGTTAATCAAGGATCTGCATTTTG	3000
Db	44208	TTCTCAGATGGTGAAGGAGAGGAAGAGCAGTTTGGGTTAATCAAGGATCTGCATTTTG	44150
QY	3001	GGACATGTTAAAGTTTGAGATTTCCAGTTCAGGCTTCCAAAGTGGTGAGGCCACATAGGCAGTT	3060
Db	44149	GGACATGTTAAAGTTTGAGATTTCCAGTTCAGGCTTCCAAAGTGGTGAGGCCACATAGGCAGTT	44090
QY	3061	CAGTGTAGAAATTCAGGACCAAGGCTGGGCA CGGTGGTCTCACTTGTGTAATCCCAGCACT	3120
Db	44089	CAGTGTAGAAATTCAGGACCAAGGCTGGGCA CGGTGGTCTCACTTGTGTAATCCCAGCACT	44030
QY	3121	TTGCTGGCTGAGCGCAGGTAGATCATTTGAGGTTCAGAGTTTCAGACAAGCTTTGGCCAA	3180
Db	44029	TTGCTGGCTGAGCGCAGGTAGATCATTTGAGGTTCAGAGTTTCAGACAAGCTTTGGCCAA	43970
QY	3181	TGCTGAAAACCCCATGCTCTACTAAAAATACAAAAATTTAGCCTGTGTGGTGGCGCAGCT	3240
Db	43969	TGCTGAAAACCCCATGCTCTACTAAAAATACAAAAATTTAGCCTGTGTGGTGGCGCAGCT	43910
QY	3241	ATAGTCCCAAGGTTTTCAGAGGCTTAGGTAGGAGAAATCCCTTTGAACCCAGGAGGTGCAGG	3300
Db	43909	ATAGTCCCAAGGTTTTCAGAGGCTTAGGTAGGAGAAATCCCTTTGAACCCAGGAGGTGCAGG	43850
QY	3301	TTGCGAGTGAGCTGAGATTTGTGCCACTGCCACTGGGTGGGTAGAGTGAGACTCTCT	3360
Db	43849	TTGCGAGTGAGCTGAGATTTGTGCCACTGCCACTGGGTGGGTAGAGTGAGACTCTCT	43790
QY	3361	CTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA	3420
Db	43789	CTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA	43730
QY	3421	TCTAAATTTGCCCTGAGCAACCACTCCTGAGTTCAA CTACCTGGGTAGACACACCTTTAAC	3480
Db	43729	TCTAAATTTGCCCTGAGCAACCACTCCTGAGTTCAA CTACCTGGGTAGACACACCTTTAAC	43670
QY	3481	ATTTTCTAGATCCACAGCTTTTAGTGAGTCTGTCTAATCATGATGATTTTGGAAATAGGAT	3540
Db	43669	ATTTTCTAGATCCACAGCTTTTAGTGAGTCTGTCTAATCATGATGATTTTGGAAATAGGAT	43610
QY	3541	CTGGGGGAGTGAGGGGGTGGCAGCCACTGTGGCAGAGAAAGACACACAGGAAAGAGC	3600
Db	43609	CTGGGGGAGTGAGGGGGTGGCAGCCACTGTGGCAGAGAAAGACACACAGGAAAGAGC	43550
QY	3601	ACCCAGGACTGTCTATATGGAGAAAGACAGGACTCCAACTACCTTCTCAAAAAATAGGA	3660



Db	43549	ACCAGAC	TGTCATATGGAAGAAACAGAGACTGCAACTCACCTTCA	CAAAATGAGGA	43499
Qy	3661	CCAGACACACGCTGATGATATGAGTTGATGCAGAGTGTTGGAGCCTCAACATCCTGCTCCC			3720
Db	43489	CCAGACACACGCTGATGGTATGAGTTGATGCAGAGTGTTGGAGCCTCAACATCCTGCTCCC			43430
Qy	3721	CTCCTACTACACATGTTTAAGGCTGTGCTCTGCTCTCAGGTTCACACTCTCTGCACATA			3780
Db	43429	CTCCTACTACACATGTTTAAGGCTGTGCTCTGCTCTCAGGTTCACACTCTCTGCACATA			43370
Qy	3781	CCCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGCTTTCTTCTGTTTGAAGCTTTGGGCTA			3840
Db	43369	CCCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGCTTTCTTCTGTTTGAAGCTTTGGGCTA			43310
Qy	3841	CGTGGATGACAGCTGTTTCGTGTTCTATGATCATGAGAGTCGCCGTGTGGAGCCCCGAAC			3900
Db	43309	CGTGGATGACAGAGCTGTTTCGTGTTCTATGATCATGAGAGTCGCCGTGTGGAGCCCCGAAC			43250
Qy	3901	TCCATGGGTTTCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA			3960
Db	43249	TCCATGGGTTTCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTCTGAA			43190
Qy	3961	AGGGTGGGATCACATGTTTCACTGTTGACACTCTGGACTATTAATGGAANAATCACAAACACAG			4020
Db	43189	AGGGTGGGATCACATGTTTCACTGTTGACACTCTGGACTATTAATGGAANAATCACAAACACAG			43130
Qy	4021	CAAGGTTATGTCGAGAGGGGGCCTCACCTTCTCTGAGGTTGTCAGAGCTTTTCATCTTTTC			4080
Db	43129	CAAGGTTATGTCGAGAGGGGGCCTCACCTTCTCTGAGGTTGTCAGAGCTTTTCATCTTTTC			43070
Qy	4081	ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCCTGTGGGAGCAGGGAAGAGGGAAG			4140
Db	43069	ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCCTGTGGGAGCAGGGAAGAGGGAAG			43010
Qy	4141	GAATTTGCTTCTCGAGATCATTTTGGTTCCTTGGGGAATGTTGGGAATAGGGA			4200
Db	43009	GAATTTGCTTCTCGAGATCATTTTGGTTCCTTGGGGAATGTTGGGAATAGGGA			42950
Qy	4201	TGGTTGCAGTTAAACAGGCTGGGGATTTTTCCAGAGTCCCACACCTTCAGGTCATCTG			4260
Db	42949	TGGTTGCAGTTAAACAGGCTGGGGATTTTTCCAGAGTCCCACACCTTCAGGTCATCTG			42890
Qy	4261	GGCTGTGAAATGCAAGAAGACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGG			4320
Db	42889	GGCTGTGAAATGCAAGAAGACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGG			42830
Qy	4321	CAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGACGACGAGAACCCAGGGCC			4380
Db	42829	CAGGACCACTTGAATTTCTGCCCTGACACACTGGATTGGAGACGACGAGAACCCAGGGCC			42770
Qy	4381	TGGCCCCAACAGCTGGAGTGGGAAAGGCAAGATTCGGGGCCAGGACAGAACAGGSCCTAC			4440
Db	42769	TGGCCCCAACAGCTGGAGTGGGAAAGGCAAGATTCGGGGCCAGGACAGAACAGGSCCTAC			42710
Qy	4441	CTGGAGAGGACCTGCCCTGACACAGCTGCAGAGTTGCTGGAGCTGGGAGAGGTTGTTTG			4500
Db	42709	CTGGAGAGGACCTGCCCTGACACAGCTGCAGAGTTGCTGGAGCTGGGAGAGGTTGTTTG			42650
Qy	4501	GACCAACAAGGTTATGTTGGAAAACAACATTTCTGCCCTTACTCTATGTGGCAGAGTGGAGG			4560
Db	42649	GACCAACAAGGTTATGTTGGAAAACAACATTTCTGCCCTTACTCTATGTGGCAGAGTGGAGG			42590
Qy	4561	AGGTTGCAGGGCAGGAAATCCCTGGTTGGAGTTTCAGAGGTGGCTGGAGCTGTGTGCCTC			4620
Db	42589	AGGTTGCAGGGCAGGAAATCCCTGGTTGGAGTTTCAGAGGTGGCTGGAGCTGTGTGCCTC			42530
Qy	4621	TCCAAATTTCTGGAAAGGACTTTCTCAATCCTAGAGTCTCTACCTTAATTTGAGATGTA			4680
Db	42529	TCCAAATTTCTGGAAAGGACTTTCTCAATCCTAGAGTCTCTACCTTAATTTGAGATGTA			42470
Qy	4681	TGAGACAGCCACAAGTCATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAAAGGAA			4740
Db	42469	TGAGACAGCCACAAGTCATGGGTTTAATTTCTTTTCTCCATGCATATGGCTCAAAAGGAA			42410

Qy	4741	GTGCTATAGGCCCTTCCTCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTTAA	4800
Db	42409	GTGCTATAGGCCCTTCCTCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTTAA	42350
Qy	4801	AAATTTCAGAAATCTCAAGGCCGGGCACGGTGGCTCACCCCTCTGAATCCCGACACTTTGGG	4860
Db	42349	AAATTTCAGAAATCTCAAGGCCGGGCACGGTGGCTCACCCCTCTGAATCCCGACACTTTGGG	42290
Qy	4861	AGCCCGAGGCGGGTGGTCTACAAGGTCAGGAGTTTGAGACCAAGCTGACCAACATGGTGAA	4920
Db	42289	AGCCCGAGGCGGGTGGTCTACAAGGTCAGGAGTTTGAGACCAAGCTGACCAACATGGTGAA	42230
Qy	4921	ACCGTCTCTTAAAAAATACAAAAATTTAGCTGGTCACAGTCATGCGCACCTGTAGTCCCA	4980
Db	42229	ACCGTCTCTTAAAAAATACAAAAATTTAGCTGGTCACAGTCATGCGCACCTGTAGTCCCA	42170
Qy	4981	GCTAAATTGGAAGCTCAGGC	5000
Db	42169	GCTAAATTGGAAGCTCAGGC	42150
RESULT 12			
AAA96794			
ID	AAA96794 standard; cDNA; 12146 BP.		
XX	AAA96794;		
AC			
XX			
XX			
DT	19-FEB-2001 (first entry)		
XX	Genomic DNA of a histocompatibility iron loading (HFE) gene.		
DE			
XX			
KW	Human; histocompatibility iron loading protein; HFE protein;		
KW	major histocompatibility complex; non-classical class I gene;		
KW	chromosome 6p; iron disorder; haemochromatosis; ss.		
XX			
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
FT	exon	1028..1324	
FT		/*tag= a	
FT		/number= 1	
FT	intron	1325..4651	
FT		/*tag= b	
FT		/number= 1	
FT	exon	4652..4915	
FT		/*tag= c	
FT		/number= 2	
FT	intron	4916..5124	
FT		/*tag= d	
FT		/number= 2	
FT	exon	5125..5400	
FT		/*tag= e	
FT		/number= 3	
FT	intron	5401..6493	
FT		/*tag= f	
FT		/number= 3	
FT	exon	6494..6769	
FT		/*tag= g	
FT		/number= 4	
FT	intron	6770..6927	
FT		/*tag= h	
FT		/number= 4	
FT	exon	6928..7041	
FT		/*tag= i	
FT		/number= 5	
FT	intron	7042..7994	
FT		/*tag= j	
FT		/number= 5	
FT	exon	7995..9050	
FT		/*tag= k	
FT		/number= 6	
FT	intron	9051..10205	

RESULT 12	
AAA96794	
ID AAA96794	standard; cDNA; 12146 BP.
XX	
XX	
AC	AAA96794;
XX	
XX	
DT	19-FEB-2001 (first entry)
XX	
XX	
DE	Genomic DNA of a histocompatibility iron loading (HFE) gene.
XX	
XX	
KW	Human; histocompatibility iron loading protein; HFE protein;
KW	major histocompatibility complex; non-classical class I gene
KW	chromosome 6p; iron disorder; haemochromatosis; ss.
XX	
OS	Homo sapiens.



FT exon /\*tag= 1  
 FT /number= 6  
 FT 10206..110637  
 FT /\*tag= m  
 PN WO200058515-A1.  
 XX  
 PD 05-OCT-2000.  
 XX  
 PF 24-MAR-2000; 2000WO-US007982.  
 XX  
 PF 26-MAR-1999; 99US-00277457.  
 XX  
 PF (BILL-) BILLUPS-ROTHENBERG INC.  
 XX  
 PI Rothenberg BE, Sawada-Hirai R, Barton JC;  
 XX WPI; 2000-647244/62.  
 DR  
 XX  
 PT Diagnosing an iron disorder e.g. hemochromatosis or a genetic  
 PT susceptibility to develop it, by determining the presence of a mutation  
 PT in exon 2 or an intron of a histocompatibility iron loading nucleic acid.  
 XX  
 PS Example 1; Page 21-28; 55pp; English.  
 CC The present sequence represents the human histocompatibility iron loading  
 CC (HFE) gene. The HFE gene is a major histocompatibility (MHC) non-  
 CC classical class I gene located on chromosome 6p. Mutations in the gene  
 CC lead to iron disorders. The specification describes a method for  
 CC diagnosing an iron disorder or a genetic susceptibility to develop the  
 CC disorder in a mammal. The method comprises determining the presence of a  
 CC mutation in exon 2 or an intron of a HFE gene or protein. The mutation is  
 CC not a C to G missense mutation at nucleotide 187 of the sequence given in  
 CC A96769 (Genbank Accession number U60319). The presence of the mutation  
 CC indicates the disorder or the genetic susceptibility to the disorder. The  
 CC method is used to diagnose an iron disorder e.g. haemochromatosis, or a  
 CC genetic susceptibility to develop it  
 XX  
 SQ Sequence 12146 BP; 3383 A; 2474 C; 2911 G; 3378 T; 0 U; 0 Other;  
 Query Match 99.1%; Score 4957.2; DB 3; Length 12146;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 4995; Conservative 0; Mismatches 3; Indels 6; Gaps 3;  
 QY 1 TCTAAGTTGAGATAAAATTTTAAATGATGATGAAATTTTGAATAATCATAAATATTTA 60  
 DB 889 TCTAAGTTGAGATAAAATTTTAAATGATGATGAAATTTTGAATAATCATAAATATTTA 948  
 QY 61 AATATCTAAAGTTTCAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACACACCCCT 120  
 DB 949 AATATCTAAAGTTTCAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACACACCCCT 1008  
 QY 121 TCAGGTTTAAACCAAGGGGACACTGGATCAGTGTGTTTCAAGGAGGTACCTT 180  
 DB 1009 TCAGGTTTAAACCAAGGGGACACTGGATCAGTGTGTTTCAAGGAGGTACCTT 1068  
 QY 181 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTTGCTTTTCAACAGAGGTT 240  
 DB 1069 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTTGCTTTTCAACAGAGGTT 1128  
 QY 241 TTACTGGGATCTCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCG 300  
 DB 1129 TTACTGGGATCTCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCG 1188  
 QY 301 TTTCGCCGCCCCCAAAAGAGCGAGATTTAAACGGGACGTCGCGCCAGAGCTGGGAA 360  
 DB 1189 TTTCGCCGCCCCCAAAAGAGCGAGATTTAAACGGGACGTCGCGCCAGAGCTGGGAA 1248  
 QY 361 ATGGGCGCCGAGCCAGGCGCGCTTCTCCTCGATGCTTTTTCAGACCGCGGTCCTG 420  
 DB 1249 ATGGGCGCCGAGCCAGGCGCGCTTCTCCTCGATGCTTTTTCAGACCGCGGTCCTG 1308  
 QY 421 CAGGGCGCTTGCTGCTGAGTCCGAGGGCTGCGGGCGAACTAGGGGCGCGGGGTG 480

DB 1309 CAGGGCGCTTGCTGCTGAGTCCGAGGGCTGCGGGCGGCGGGGTG 1368  
 QY 481 GAAAAATCGAAACTAGCTTTTTCCTGCGCTTGGAGTTTGTCTAACTTTGGAGGACTGTC 540  
 DB 1369 GAAAAATCGAAACTAGCTTTTTCCTGCGCTTGGAGTTTGTCTAACTTTGGAGGACTGTC 1428  
 QY 541 TCAACCCCTATCGCAAGCCCTCTCCCTACTTTCTGCGTCCAGACCCCGGTAGGGAGTGC 600  
 DB 1429 TCAACCCCTATCGCAAGCCCTCTCCCTACTTTCTGCGTCCAGACCCCGGTAGGGAGTGC 1488  
 QY 601 CTACCACTGAACTGCAAGTGGGGTCCCTGCGCCCAAGGACCTGCCCCCTCCCGGCTGT 660  
 DB 1489 CTACCACTGAACTGCAAGTGGGGTCCCTGCGCCCAAGGACCTGCCCCCTCCCGGCTGT 1548  
 QY 661 CCGGGCTGCGGAGTGACTTTTGGNAACCGCCCACTCCCTTCCCTCCCACTAGATGCTTT 720  
 DB 1549 CCGGGCTGCGGAGTGACTTTTGGNAACCGCCCACTCCCTTCCCTCCCACTAGATGCTTT 1608  
 QY 721 TAAATAAATCTCGTAGTTCTCTCACTTGAAGTAAAGCTGAGGCTGCGGGCTCTTGAACCTGG 780  
 DB 1609 TAAATAAATCTCGTAGTTCTCTCACTTGAAGTAAAGCTGAGGCTGCGGGCTCTTGAACCTGG 1668  
 QY 781 AACTCGGGTTAATTTCCAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
 DB 1669 AACTCGGGTTAATTTCCAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1728  
 QY 841 AAGTTCTTCCCTGAGTGTCTGCGGAGAGGCTGAGCAAAACCCACAGCAGATCCGACCG 900  
 DB 1729 AAGTTCTTCCCTGAGTGTCTGCGGAGAGGCTGAGCAAAACCCACAGCAGATCCGACCG 1788  
 QY 901 GGTTCACCTCAGAACAAATGCTGCTGCGGGCGCGGAGAGTGGGCTTGGGGA 960  
 DB 1789 GGTTCACCTCAGAACAAATGCTGCTGCGGGCGCGGAGAGTGGGCTTGGGGA 1848  
 QY 961 TCTGAATTTTCCACCAATTTCCACCAATTTTGGTGAGACCTGGGGTGGAGGTCTTAGGGT 1020  
 DB 1849 TCTGAATTTTCCACCAATTTCCACCAATTTTGGTGAGACCTGGGGTGGAGGTCTTAGGGT 1908  
 QY 1021 GGGAGGCTCTGAGAGAGGCTTACCTCGGGCTTTTCCCACTTTGGGCAATTTGTTCTTT 1080  
 DB 1909 GGGAGGCTCTGAGAGAGGCTTACCTCGGGCTTTTCCCACTTTTGGGCAATTTGTTCTTT 1968  
 QY 1081 GCTCGAAAAATTAAGTATATGTTAGTTTGAACCTTGAACCTGAACTGAACTCTCTTTTCGG 1140  
 DB 1969 GCTCGAAAAATTAAGTATATGTTAGTTTGAACCTTGAACCTGAACTGAACTCTCTTTTCGG 2028  
 QY 1141 CTAGGCTTTATGATTTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200  
 DB 2029 CTAGGCTTTATGATTTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2088  
 QY 1201 TAAATGAACATGTAAGCAATGCACTTCTAAGTTTACATTTTACATTTCTTATTTTCA 1260  
 DB 2089 TAAATGAACATGTAAGCAATGCACTTCTAAGTTTACATTTTACATTTCTTATTTTGA 2148  
 QY 1261 TTTTCACTAGGATAGGAGGTAGGAGCTAAATACTGTTTATTTTACTAGAGTTAACT 1320  
 DB 2149 TTTTCACTAGGATAGGAGGTAGGAGCTAAATACTGTTTATTTTACTAGAGTTAACT 2208  
 QY 1321 GGAATTCAGATTTATTAATCTTTTTCAGGTTTCAAAAGAACATAAATAAATCTGGTTTCTG 1380  
 DB 2209 GGAATTCAGATTTATATACTTTTTCAGGTTTCAAAAGAACATAAATAAATCTGGTTTCTG 2268  
 QY 1381 ATGTTATTTCAAGTACTAGCTGCTTCTAATCTTAGTTTGAAGTATTTTGGCTGTAG 1440  
 DB 2269 ATGTTATTTCAAGTACTAGCTGCTTCTAATCTTAGTTTGAAGTATTTTGGCTGTAG 2328  
 QY 1441 TGTAGCAGAGTGTCTGTTGGGTCAACCGCGGCTCAGCACAGCACTTTGAGTTTGGTA 1500  
 DB 2329 TGTAGCAGAGTGTCTGTTGGGTCAACCGCGGCTCAGCACAGCACTTTGAGTTTGGTA 2388  
 QY 1501 CTACGTTATCCACATTTTACATGACAAAGATGAGGCATGGCAGCGCTCTCTCTCTG 1560



2389	Db	CTACGTGTATCCACATTTTATACATGACAGAAATGAGGCATGGCAGCGCCCTGCTCTCTCGG	2444
1561	Qy	CAAAATTTATTTCAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTTCATPAGC	1620
2449	Db	CAAAATTTATTTCAATGGTACACGGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTTCATAGC	2508
1621	Qy	TATGATTTCTTAAACATCACACTGCATGTAGAGTTGAATAATAAAATTCATGTGAGCAG	1680
2509	Db	TATGATTTCTTAAACATCACACTGCATGTAGAGTTGAATAATAAAATTCATGTGAGCAG	2568
1681	Qy	AAATATTTCAATTTGTATCAAGTGTAAATGAGTCCAGCCATGTGTGACACTGTTTCAAGCCC	1740
2569	Db	AAATATTTCAATTTGTATCAAGTGTAAATGAGTCCAGCCATGTGTGACACTGTTTCAAGCCC	2628
1741	Qy	CAAGGAGAGACGACGGGAAAACAAGTCTTTTACCCTTTTGATATTTTGTGATTTCTAGTGGGAGA	1800
2629	Db	CAAGGAGAGACGAGGGGAAAACAAGTCTTTTACCCTTTTGATATTTTGTGATTTCTAGTGGGAGA	2688
1801	Qy	GATGACAAATGAAGCAAAATGAGCAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA	1860
2689	Db	GATGACAAATGAAGCAAAATGAGCAGAAAGATATACAACATCAGGAAATCATGGGTGTTGTGA	2748
1861	Qy	GAAGCAGAGAAAGTCAGGGCAAGTCACCTCTGGGGCTGACACTTGAAGCAGACATGAAGGA	1920
2749	Db	GAAGCAGAGAAAGTCAGGGCAAGTCACCTCTGGGGCTGACACTTGAAGCAGACATGAAGGA	2808
1921	Qy	AATAAAGAAATGATATTGACTGGAGCAGTATTTCCAGGCAGAACTGAGTGGGCCCTGGCAAG	1980
2809	Db	AATAAAGAAATGATATTGACTGGAGCAGTATTTCCAGGCAGAACTGAGTGGGCCCTGGCAAG	2868
1981	Qy	TTGGATTTAAAAAGCGGGTTTTTCTCAGCACTACTCATGTGTGTGTGTGTGGGGGGGGGGG	2040
2869	Db	TTGGATTTAAAAAGCGGGTTTTTCTCAGCACTACTCATGTGTGTGTGTGTGGGGGGGGGGG	2927
2041	Qy	CGGCGTGGGGGTGGGAAGGGGGACTACCATCTGCATGTAGCATGTCTAGCAGATATCCTGT	2100
2928	Db	CGGCGTGGGGGTGGGAAGGGGGACTACCATCTGCATGTAGCATGTCTAGCAGATATCCTGT	2987
2101	Qy	CCTCCCTACTCACATGAGTGTCTAGGAGCACTCCCCAGTCTTTGACCAACCAAAAATGTCTCT	2160
2988	Db	CCTCCCTACTCACATGAGTGTCTAGGAGCACTCCCCAGTCTTTGACCAACCAAAAATGTCTCT	3047
2161	Qy	AAACTTTGCCACATGTCACCTAGTAGACAAACTCCTGTGTTAAGAAGCTCGGGTTGAAAAA	2220
3048	Db	AAACTTTGCCACATGTCACCTAGTAGACAAACTCCTGTGTTAAGAAGCTCGGGTTGAAAAA	3107
2221	Qy	AATAAACAGATGATGCTGGGAGTAGAGGCCAAGAAGTAGGTAAATGGGCTCAGAAAGGA	2280
3108	Db	AATAAACAGATGATGCTGGGAGTAGAGGCCAAGAAGTAGGTAAATGGGCTCAGAAAGGA	3167
2281	Qy	GCCACAAACAGGTGTGACGGCGCCTGTAGGCTGTGTGATTTCTAGCCCAAGGAGTA	2340
3168	Db	GCCACAAACAGGTGTGACGGCGCCTGTAGGCTGTGTGATTTCTAGCCCAAGGAGTA	3227
2341	Qy	ACAGTGATCTGTACAGGCCTTTTAAAAAGATTGCTCTGGCTGCTATGTGGAAGCAGAAATG	2400
3228	Db	ACAGTGATCTGTACAGGCCTTTTAAAAAGATTGCTCTGGCTGCTATGTGGAAGCAGAAATG	3287
2401	Qy	AAGGGAGCAACAGTAAAGCAGGGAGCCCAAGCAAGGAAGCTGTTTACACAGTCCAGGCAAG	2460
3288	Db	AAGGGAGCAACAGTAAAGCAGGGAGCCCAAGCAAGGAAGCTGTTTACACAGTCCAGGCAAG	3347
2461	Qy	AGGTAGTGGAGTGGGCTGGGTGGGAAACAGAAAGGGAGTCACAAACATTTGCTCTCTGAA	2520
3348	Db	AGGTAGTGGAGTGGGCTGGGTGGGAAACAGAAAGGGAGTCACAAACATTTGCTCTCTGAA	3407
2521	Qy	TATATTTCTGAAGGAATTTGCTGAAGGATTTCTATGTTGTGTGAGAGAAAGAGAAATTTGG	2580
3408	Db	TATATTTCTGAAGGAATTTGCTGAAGGATTTCTATGTTGTGTGAGAGAAAGAGAAATTTGG	3467
2581	Qy	CTGGGTGTAGTGTCTATGCCAGAGGAGGAGCCCAAGGAGACAGATTCCTGAGCTCAGGA	2640
3468	Db	CTGGGTGTAGTGTCTATGCCAGAGGAGGAGCCCAAGGAGACAGATTCCTGAGCTCAGGA	3527

QY	2641	GTTCAGAGCAGCCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAAATACAAAAATT	2700
DB	3528	GTTCAGAGCAGCCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAAATACAAAAATT	3587
QY	2701	GCTGGGTGTGGTGCCATGCACCTGTGTACTCTAGCTACTCGGGAGGCTGAGGTGGAGGTA	2760
DB	3588	GCTGGGTGTGGTGCCATGCACCTGTGTACTCTAGCTACTCGGGAGGCTGAGGTGGAGGTA	3647
QY	2761	TTGCTTGAGCCCAAGAAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTCACG	2820
DB	3648	TTGCTTGAGCCCAAGAAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTCACG	3707
QY	2821	CTAGGTCACAGCAAGCAACCCCTGTCTCCCTGACCCCTGAAAGAGAGAGAGTTAAAGT	2880
DB	3708	CTAGGTCACAGCAAGCAACCCCTGTCTCCCTGACCCCTGAAAGAGAGAGAGTTAAAGT	3767
QY	2881	TGACTTTTGTCTTTATTTATTTTAAATTTATTTGCCCTGAGCAGTGGGTAAATTTGCCAATGCCAT	2940
DB	3768	TGACTTTTGTCTTTATTTATTTTAAATTTATTTGCCCTGAGCAGTGGGTAAATTTGCCAATGCCAT	3827
QY	2941	TTCTGAGATGGTGAAGCAGAGAAAGACAGACAGTTTGGGGTAAATCAAGGATCTGCATTTG	3000
DB	3828	TTCTGAGATGGTGAAGCAGAGAAAGACAGACAGTTTGGGGTAAATCAAGGATCTGCATTT-	3886
QY	3001	GGACATGTTAAGTTTGGAGTTTCCAGTCAGGCTTCCAAGTGGTCAGGCCACATAGGCGAGTT	3060
DB	3887	GGACATGTTAAGTTTGGAGTTTCCAGTCAGGCTTCCAAGTGGTCAGGCCACATAGGCGAGTT	3946
QY	3061	CAGTGTGAAGAAATTCAGGACCAAGGCTGGGCAACGGTGGCTCACTTGTGTAATCCAGCACT	3120
DB	3947	CAGTGTGAAGAAATTCAGGACCAAGGCAACGGTGGCTCACTTGTGTAATCCAGCACT	4006
QY	3121	TTGGTGGCTCAGGCAGGCTAGATCATTTTGGGTCAGGAGTTTGGAGACAAGCTTGGCCAAACA	3180
DB	4007	TTGGTGGCTCAGGCAGGCTAGATCATTTTGGGTCAGGAGTTTGGAGACAAGCTTGGCCAAACA	4066
QY	3181	TGGTGAACACCCATGTCTACTTAAATAATACAAAAATTAGCCTGGTGGTGGCGCAGCGCT	3240
DB	4067	TGGTGAACACCCATGTCTACTTAAATAATACAAAAATTAGCCTGGTGGTGGCGCAGCGCT	4126
QY	3241	ATAGTCCACGGTTTTTCAGGAGGCTTAGTGAGGAGATCCCTTCGAACCCAGGAGGTGCAGG	3300
DB	4127	ATAGTCCACGGTTTTTCAGGAGGCTTAGTGAGGAGATCCCTTCGAACCCAGGAGGTGCAGG	4186
QY	3301	TTGCAGTGCAGCTGAGATTGTGCCACTGCACTCCAGCCTGGGTATAGAGTGAAGACTCTGT	3360
DB	4187	TTGCAGTGCAGCTGAGATTGTGCCACTGCACTCCAGCCTGGGTATAGAGTGAAGACTCTGT	4246
QY	3361	CTC-----AAAAAAAAAAAAAAAAAAAAAAAACTGAAGGAAATTATTCTCTCAGGATT	3416
DB	4247	CTCAAAAAAAAAAAAAAAAAAAAAAAAACTGAAGGAAATTATTCTCTCAGGATT	4306
QY	3417	TGGGTCTAAATTGGCCCTGAGCACCAACTCTGTAGTTTCAACTACCATGGCTAGACACACCT	3476
DB	4307	TGGGTCTAAATTGGCCCTGAGCACCAACTCTGTAGTTTCAACTACCATGGCTAGACACACCT	4366
QY	3477	TAACATTTTCTAGAAATCCACAGCTTTAGTGGAGTCTGTCTAATCATAGAGTATTGGAATA	3536
DB	4367	TAACATTTTCTAGAAATCCACAGCTTTAGTGGAGTCTGTCTAATCATAGAGTATTGGAATA	4426
QY	3537	GGATCTGGGGCAGTGAGGGGGTGGCAGCACTGTGGCAGAGAAAGACACAAAGAAA	3596
DB	4427	GGATCTGGGGCAGTGAGGGGGTGGCAGCACTGTGGCAGAGAAAGACACAAAGAAA	4486
QY	3597	GAGCACCCAGGACTGTCTATATGGAAGAAAAGACAGGACTGCAACTTCAACCTTCAAAAATG	3656
DB	4487	GAGCACCCAGGACTGTCTATATGGAAGAAAAGACAGGACTGCAACTTCAACCTTCAAAAATG	4546
QY	3657	AGGACACAGACACAGCTGATGGTATAGTTGATGACGAGTGTGTGGAGGCTTCAATCTCTGC	3716
DB	4547	AGGACACAGACACAGCTGATGGTATAGTTGATGACGAGTGTGTGGAGGCTTCAATCTCTGC	4606



QY 3717 TCCCTCCTACTACTACATAGTTAAGGCTGTGCTCTGCTCTCAGGTTTCACTCTCTGC 3776  
DB TCCCTCCTACTACTACATAGTTAAGGCTGTGCTCTGCTCTCAGGTTTCACTCTCTGC 4666  
QY 3777 ACTACCTCTTTCATGGGTGCTCAGACAGACCTTGGTCTTCTTCTTCTTGAAGCTTTGG 3836  
DB ACTACCTCTTTCATGGGTGCTCAGACAGACCTTGGTCTTCTTCTTCTTGAAGCTTTGG 4726  
QY 3837 GCTACGTGATGACCAAGCTTCTGCTTCTATGATCATGAGAGTCGCGCTGTGGAGCCCC 3896  
DB GCTACGTGATGACCAAGCTTCTGCTTCTATGATCATGAGAGTCGCGCTGTGGAGCCCC 4786  
QY 3897 GAATCTCATGGGTTTCCAGTAGAATTTCAAGCAGATGTGGCTGCGAGCTGAGTCAGAGTC 3956  
DB GAATCTCATGGGTTTCCAGTAGAATTTCAAGCAGATGTGGCTGCGAGCTGAGTCAGAGTC 4846  
QY 3957 TGAAGGGTGGGATCACATGTTCACTGTTGACITCTGGACTATATGGAATATCAACACC 4016  
DB TGAAGGGTGGGATCACATGTTCACTGTTGACITCTGGACTATATGGAATATCAACACC 4906  
QY 4017 ACAGCAAGGATGTGTGGAGAGGGGCTCACCTTCTGAGGTTGTGAGAGCTTTTCATCT 4076  
DB ACAGCAAGGATGTGTGGAGAGGGGCTCACCTTCTGAGGTTGTGAGAGCTTTTCATCT 4966  
QY 4077 TTTTCATGCTTTGAAGGAAACAGCTGGAAGTCTGAGGTTGTGGAGCAGGAAGAGG 4136  
DB TTTTCATGCTTTGAAGGAAACAGCTGGAAGTCTGAGGTTGTGGAGCAGGAAGAGG 5026  
QY 4137 GAAGGAATTTGCTTCTGAGATCATTTGCTTCTGGGATGTGGAAATAGGACCTATT 4196  
DB GAAGGAATTTGCTTCTGAGATCATTTGCTTCTGGGATGTGGAAATAGGACCTATT 5086  
QY 4197 CTTTCTGCTTCAAGGCTGCGGATTTTTCAGAGTCCACACCTCGAGGTCAT 4256  
DB CTTTCTGCTTCAAGGCTGCGGATTTTTCAGAGTCCACACCTCGAGGTCAT 5146  
QY 4257 CTGCGCTGTGAATGCAAGAGAACACAGTACCGAGGCTACTGGAAGTACGGTATGA 4316  
DB CTGCGCTGTGAATGCAAGAGAACACAGTACCGAGGCTACTGGAAGTACGGTATGA 5206  
QY 4317 TGGGAGGACCACTTTGAAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAACCCAG 4376  
DB TGGGAGGACCACTTTGAAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAACCCAG 5266  
QY 4377 GGCCTGCCCCACCAAGCTGAGTGGGAAGGCAAGATTTCCGGCCAGCAGCAACAGGCG 4436  
DB GGCCTGCCCCACCAAGCTGAGTGGGAAGGCAAGATTTCCGGCCAGCAGCAACAGGCG 5326  
QY 4437 CTACTGGAGAGGACTGCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGAGAGGTG 4496  
DB CTACTGGAGAGGACTGCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGAGAGGTG 5386  
QY 4497 TTTGGACCAACAGGTATGTTGGTGAACACACTTCTGCCCTTATCTCTAGTGGCAGAGTG 4556  
DB TTTGGACCAACAGGTATGTTGGTGAACACACTTCTGCCCTTATCTCTAGTGGCAGAGTG 5386  
QY 4557 GAGGAGGTTGCGGGCAGCGAATCCTGCTTGGAGTTTCAGAGGTGCGCTGAGGCTGTG 4616  
DB GAGGAGGTTGCGGGCAGCGAATCCTGCTTGGAGTTTCAGAGGTGCGCTGAGGCTGTG 5506  
QY 4617 CTTCTCAAATTTCTGGGAAGGACTTTCTCAATCTCTAGAGTCTCTACCTTATAATTGAGA 4676  
DB CTTCTCAAATTTCTGGGAAGGACTTTCTCAATCTCTAGAGTCTCTACCTTATAATTGAGA 5566  
QY 4677 TGTATGAGCAGCCACAGTCATGGGTTTAATTTCTTTTCTCCATGTCATATGCTCAAG 4736  
DB TGTATGAGCAGCCACAGTCATGGGTTTAATTTCTTTTCTCCATGTCATATGCTCAAG 5626  
QY 4737 GGAAGTGTCTATGGCCCTTGTCTTTTATTTTAAACCAATAATCTTTTGTATATTTATACCTG 4796  
DB GGAAGTGTCTATGGCCCTTGTCTTTTATTTTAAACCAATAATCTTTTGTATATTTATACCTG 5686  
QY 4797 TTAATAAATTCAGAAATGTCAAGCGCGGACGCTGCTCACCCCTGTATATCCAGCATT 4856

DB 5687 TTAATAAATTCAGAAATGTCAAGCGCGGACGCTGCTCACCCCTGTATATCCAGCATT 5746  
QY 4857 TGGGAGGCGGAGCGGCTGTGTCACAGGTCAGAGTTTGAGACCGCTGACCAACATGG 4916  
DB 5747 TGGGAGGCGGAGCGGCTGTGTCACAGGTCAGAGTTTGAGACCGCTGACCAACATGG 5806  
QY 4917 TGAACCCCTCTCTAAAAAATAAAAAATAGCTGCTCAGTCATGCGCACCCTGTAGT 4976  
DB 5807 TGAACCCCTCTCTAAAAAATAAAAAATAGCTGCTCAGTCATGCGCACCCTGTAGT 5866  
QY 4977 CCAGCTAATTTGGAAGCTGAGGC 5000  
DB 5867 CCAGCTAATTTGGAAGCTGAGGC 5890

RESULT 13  
AAV57903/c  
ID AAV57903 standard; DNA; 237326 BP.  
XX  
AC AAV57903;  
XX  
DT 21-DEC-1998 (first entry)  
XX  
DE Hereditary haemochromatosis subregion from an HH affected individual.  
XX  
KW Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE;  
KW diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3; BTF4;  
KW BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;  
KW type 1 sodium transport gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9814466-A1.  
XX  
PD 09-APR-1998.  
XX  
PF 30-SEP-1997; 97WO-US017658.  
XX  
PR 01-OCT-1996; 96US-00724394.  
PR 07-MAY-1997; 97US-00852495.  
XX  
PA (PROG-) PROGENITOR INC.  
XX  
PI Feder JN, Kronmal GS, Lauer PM, Ruddy DA, Thomas WJ;  
PI Tsuchihashi Z, Wolff RK;  
XX  
WI WI; 1998-240014/21.  
XX  
Hereditary haemochromatosis gene products - used to develop products for  
the diagnosis and treatment of hereditary disorders in iron metabolism.  
XX  
Claim 1; Fig 9; 209pp; English.  
XX  
The present invention describes hereditary haemochromatosis gene products  
from the human haemochromatosis gene. The present sequence represents a  
hereditary haemochromatosis subregion from an hereditary haemochromatosis  
(HH) affected individual. Also described is a method to determine the  
presence or absence of the common hereditary haemochromatosis (HFE) gene  
mutation in an individual comprising: (a) providing DNA or RNA from the  
individual; and (b) assessing the DNA or RNA for the presence or absence  
of a haplotype or genotype where the presence or absence of the haplotype  
genotype indicates the likely presence of the HFE gene mutation in the  
genome of the individual. The HFE gene sequences from the present  
invention can be used to develop products for use in the diagnosis and  
treatment of HFE. The present invention also describes BTF genes, which  
are homologues of the milk protein butyrophilin (BT), and can be used in  
the production of agonists and antagonists of BT function. Also described  
are: (1) a RoRet gene which can be used to develop products for the  
study, diagnosis and treatment of lupus and Sjogren's syndrome; and (2)  
NPT3 and NPT4 genes which are homologues of a type 1 sodium transport  
gene, and can similarly be used for hypophosphatemia  
XX







QY	2101	CTCCCTACTACTAGTGTCTAGGACACTCCCCCACTCTTGACAAACCAAAATGTCTCT	2160
Db	45002	CTCCCTACTACTAGTGTCTAGGACACTCCCCCACTCTTGACAAACCAAAATGTCTCT	44943
QY	2161	AAACTTTGGCACATGTCACCTAGTAGACAAACTCCTGGTTTAAAGAACTCGGGTTGAAAA	2220
Db	44942	AAACTTTGGCACATGTCACCTAGTAGACAAACTCCTGGTTTAAAGAACTCGGGTTGAAAA	44883
QY	2221	AATAAACAAAGTAGTGTGGGGAGTAGAGGCCAAGAAAGTAGGTAATGGGCTCAGAAAGGA	2280
Db	44882	AATAAACAAAGTAGTGTGGGGAGTAGAGGCCAAGAAAGTAGGTAATGGGCTCAGAAAGGA	44823
QY	2281	GCACAAAACAGGTTGTGACAGGCGCTGTAGGCTGTGGTGTGAATTTAGCCCAAGAGTA	2340
Db	44822	GCACAAAACAGGTTGTGACAGGCGCTGTAGGCTGTGGTGTGAATTTAGCCCAAGAGTA	44763
QY	2341	ACAGTGATCTGTACAGGCTTTTAAAGATTGCTCTGGCTGTCTATGTGGAAAGCAGAAATG	2400
Db	44762	ACAGTGATCTGTACAGGCTTTTAAAGATTGCTCTGGCTGTCTATGTGGAAAGCAGAAATG	44703
QY	2401	AAGGGAGCAACAGTAAAGCAGGAGCCACAGCCAGGAAGCTGTTACACAGTCCAGGCAAG	2460
Db	44702	AAGGGAGCAACAGTAAAGCAGGAGCCACAGCCAGGAAGCTGTTACACAGTCCAGGCAAG	44643
QY	2461	AGGTAGTGAGTGGGCTGGGTGGGAAACAGAAAAGGAGGTGACAAACCAATTTGCTCCTGAA	2520
Db	44642	AGGTAGTGAGTGGGCTGGGTGGGAAACAGAAAAGGAGGTGACAAACCAATTTGCTCCTGAA	44583
QY	2521	TATATTTCTGAAGAAAGTTGCTGAAGGATTCATATGTTGTGTGAGAGAAAGAAATTTGG	2580
Db	44582	TATATTTCTGAAGAAAGTTGCTGAAGGATTCATATGTTGTGTGAGAGAAAGAAATTTGG	44523
QY	2581	CTGGGTGTAGTACATGCAAGAGGAGGCGCAAGCAGAGCAGATTTCTTGAGCTCAGGA	2640
Db	44522	CTGGGTGTAGTACATGCAAGAGGAGGCGCAAGCAGAGCAGATTTCTTGAGCTCAGGA	44463
QY	2641	GTTCAAGACAGCCTGGGCAACACAGCAAAACCCCTTCTCTACAAAATAACAAAATTA	2700
Db	44462	GTTCAAGACAGCCTGGGCAACACAGCAAAACCCCTTCTCTACAAAATAACAAAATTA	44403
QY	2701	GCTGGGTGTGGGCAATGACCTGTGATCCTAGTACTCGGAGGCTGAGGTGGAGGTA	2760
Db	44402	GCTGGGTGTGGGCAATGACCTGTGATCCTAGTACTCGGAGGCTGAGGTGGAGGTA	44343
QY	2761	TTGCTTGAGCCACAGGAAGTTGAGGCTGAGTGCACATGCTGACCTGCTACTTTACG	2820
Db	44342	TTGCTTGAGCCACAGGAAGTTGAGGCTGAGTGCACATGCTGACCTGCTACTTTACG	44283
QY	2821	CTAGGTGACAGAGCAAGCCCTGTCTCCCTGACCCCTGAAAAAGAGAGTTAAAGT	2880
Db	44282	CTAGGTGACAGAGCAAGCCCTGTCTCCCTGACCCCTGAAAAAGAGAGTTAAAGT	44223
QY	2881	TGACTTTGTTCTTTATTTTATTTATTTGCGCTGAGCAGTGGGTAATTTGGCAATGCCAT	2940
Db	44222	TGACTTTGTTCTTTATTTTATTTTATTTGCGCTGAGCAGTGGGTAATTTGGCAATGCCAT	44163
QY	2941	TTCTGAGATGTTGAAGCTTGAAGGAGAGACAGTTTGGGGTAAATCAAGGATCTGCAATTT	3000
Db	44162	TTCTGAGATGTTGAAGCTTGAAGGAGAGACAGTTTGGGGTAAATCAAGGATCTGCAATTT	44104
QY	3001	GGACATGTTTAAAGTTTGAATTTCCAGTCCAGGCTTCCAAAGTGGTGAGGCCACATAGGCAGTT	3060
Db	44103	GGACATGTTTAAAGTTTGAATTTCCAGTCCAGGCTTCCAAAGTGGTGAGGCCACATAGGCAGTT	44044
QY	3061	CAGTGTAAAGAAATTCAGAGCAAGGCTGGGCAAGTGGCTCACTTCGTAAATCCAGCACT	3120
Db	44043	CAGTGTAAAGAAATTCAGAGCAAGGCTGGGCAAGTGGCTCACTTCGTAAATCCAGCACT	43984
QY	3121	TTGGTGGCTGAGCGAGGTAGATCATTTGAGGTCAGGATTTTGAGCAAGCTTTGGCCAA	3180
Db	43983	TTGGTGGCTGAGCGAGGTAGATCATTTGAGGTCAGGATTTTGAGCAAGCTTTGGCCAA	43924
QY	3181	TGGTGAACCCCATGTCTACTAAAAATACAAAAATTAGCCTGTGTGGTGGCGCAGCCT	3240

Db	43923	TGGTGAACCCCATGTCTACTAAAAATACAAAAATAGCCTGTGTGGTGGCGCAGCCT	43864
QY	3241	ATAGTCCCAAGGTTTTCAGGAGGCTTAGGTAGGAGAACTCCTTGAACCCAGGAGGTGACGG	3300
Db	43863	ATAGTCCCAAGGTTTTCAGGAGGCTTAGGTAGGAGAACTCCTTGAACCCAGGAGGTGACGG	43804
QY	3301	TTGCGATGAGCTGAGATTGTGCACCTGCACCTCAGCCTCGGGTGATAGAGTGAGACTCTGT	3360
Db	43803	TTGCGATGAGCTGAGATTGTGCACCTGCACCTCAGCCTCGGGTGATAGAGTGAGACTCTGT	43744
QY	3361	CTC-----AAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	3416
Db	43743	CTC-----AAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	43684
QY	3417	TGGGTCTAATTTTCCCTGAGCACCACCTCCTCAGTCTCACTACCACTGAGTGTAGCACACCT	3476
Db	43683	TGGGTCTAATTTTCCCTGAGCACCACCTCCTCAGTCTCACTACCACTGAGTGTAGCACACCT	43624
QY	3477	TAAACATTTTCTAGAATCCACACAGCTTTAGTGGAGTCTGTCTAATCATAGATTTGGAATA	3536
Db	43623	TAAACATTTTCTAGAATCCACACAGCTTTAGTGGAGTCTGTCTAATCATAGATTTGGAATA	43564
QY	3537	GGATCTGGGGGAGTGTAGGGGTGGCAGCCACGTGTGGCAGAGAAAAGCACACAGGAAA	3596
Db	43563	GGATCTGGGGGAGTGTAGGGGTGGCAGCCACGTGTGGCAGAGAAAAGCACACAGGAAA	43504
QY	3597	GAGCACCAGGACTGTCATATGGAAGAAAGACAGGACTGCAACTCACCTTCACAAAATG	3656
Db	43503	GAGCACCAGGACTGTCATATGGAAGAAAGACAGGACTGCAACTCACCTTCACAAAATG	43444
QY	3657	AGGACACAGACACAGCTGTATGAGTTGATGAGGCTGTGGAGCCTCAACATCCTGC	3716
Db	43443	AGGACACAGACACAGCTGTATGAGTTGATGAGGCTGTGGAGCCTCAACATCCTGC	43384
QY	3717	TCCCTCTCTACTACATGGTTAAGCCCTTGTCTGTCTCAGGTTCACTCTCTGC	3776
Db	43383	TCCCTCTCTACTACATGGTTAAGCCCTTGTCTGTCTCAGGTTCACTCTCTGC	43324
QY	3777	ACTACTCTTCATGGTGGCTCAGAGCAGGACTTGGTCTTCTTCTTGTGAGCTTTGG	3836
Db	43323	ACTACTCTTCATGGTGGCTCAGAGCAGGACTTGGTCTTCTTCTTGTGAGCTTTGG	43264
QY	3837	GCTAGTGGATGACACAGCTGTTTCGTGTTCTATGATCACTAGAGTCCGCTGTGGAGCCC	3896
Db	43263	GCTAGTGGATGACACAGCTGTTTCGTGTTCTATGATCACTAGAGTCCGCTGTGGAGCCC	43204
QY	3897	GAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAAGTCTC	3956
Db	43203	GAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAAGTCTC	43144
QY	3957	TGAAAAGGTGGATCACAATGTTCACTGTTGACTTCTGGACTATTATGGAATATCAACCC	4016
Db	43143	TGAAAAGGTGGATCACAATGTTCACTGTTGACTTCTGGACTATTATGGAATATCAACCC	43084
QY	4017	ACAGCAAGGTTATGTGGAGAGGGGCTCACCTCTCTGAGGTTGTGAGAGCTTTTCATCT	4076
Db	43083	ACAGCAAGGTTATGTGGAGAGGGGCTCACCTCTCTGAGGTTGTGAGAGCTTTTCATCT	43024
QY	4077	TTTTCATGCACTTTGAAGGAAACAGCTGGAAGTCTGAGGTTCTTGTGGGAGCAGGGAAGAG	4136
Db	43023	TTTTCATGCACTTTGAAGGAAACAGCTGGAAGTCTGAGGTTCTTGTGGGAGCAGGGAAGAG	42964
QY	4137	GAAAGAAATTTGCTTCTCCTGAGATCAATTTGGTCTCTGGGATGTGGAATATAGGACCTATT	4196
Db	42963	GAAAGAAATTTGCTTCTCCTGAGATCAATTTGGTCTCTGGGATGTGGAATATAGGACCTATT	42904
QY	4197	CTTTGGTGGCAATTTAAACAGGCTGGGATTTTTCAGAGTCCACACCTCAGGTCAAT	4256
Db	42903	CTTTGGTGGCAATTTAAACAGGCTGGGATTTTTCAGAGTCCACACCTCAGGTCAAT	42844
QY	4257	CCTGGGCTGTGAAATGCAAGAGAACACAGATCCGAGGCTACTCGAAGTACGGGTATGA	4316



Db 42843 CCTGGGCTGTGAATGCAAGAGACAAACAGTACCGAGGCTACTGGAAGTACGGGTATGA 42784  
QY 4317 TGGGAGGACCACTTGTGAATTCCTGCTGACACACTGGAATGGAGAGACGACCCAG 4376  
Db 42783 TGGGAGGACCACTTGAATTCCTGCTGACACACTGGAATGGAGAGACGACCCAG 42724  
QY 4377 GGCCTGGCCCAACAGCTGGAGTGGGAAGGCACAGAATTCGGGCCAGGCAGACAGGC 4436  
Db 42723 GGCCTGGCCCAACAGCTGGAGTGGGAAGGCACAGAATTCGGGCCAGGCAGACAGGC 42664  
QY 4437 CTACCTGGAGAGGAGTGCCTTCGACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTGT 4496  
Db 42663 CTACCTGGAGAGGAGTGCCTTCGACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTGT 42604  
QY 4497 TTTGACCAACAAAGTATGGTGGAAACACACTTCTGCCCTATATCTAGTGGCAGAGTG 4556  
Db 42603 TTTGACCAACAAAGTATGGTGGAAACACACTTCTGCCCTATATCTAGTGGCAGAGTG 42544  
QY 4557 GAGGAGGTTGCAGGCGACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTG 4616  
Db 42543 GAGGAGGTTGCAGGCGACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTG 42484  
QY 4617 CCTCTCCAAATTCCTGGGAAGGACTTCTCAATCCTAGAGTCTCTACCTTATATTTAGA 4676  
Db 42483 CCTCTCCAAATTCCTGGGAAGGACTTCTCAATCCTAGAGTCTCTACCTTATATTTAGA 42424  
QY 4677 TGTATGAGACGCCACAAGTCAATGCTGTTAAATTTCTTTCCTCATGCAATATGGCTCAAAG 4736  
Db 42423 TGTATGAGACGCCACAAGTCAATGCTGTTAAATTTCTTTCCTCATGCAATATGGCTCAAAG 42364  
QY 4737 GGAAGTGTATGCGCCCTGCTTTTATTTAAACCAATATCTTTTGTATATTTATACCTG 4796  
Db 42363 GGAAGTGTATGCGCCCTGCTTTTATTTAAACCAATATCTTTTGTATATTTATACCTG 42304  
QY 4797 TTAATAAATTCAGAAATGTCAAGCGCGGCACGCTGGCTCACCCCTGTAAATCCAGCACTT 4856  
Db 42303 TTAATAAATTCAGAAATGTCAAGCGCGGCACGCTGGCTCACCCCTGTAAATCCAGCACTT 42244  
QY 4857 TGGGAGGCGGAGGCGGCTGCTCAAGGTTCAGAGTGGTGGAGACAGCTGACCAACATGG 4916  
Db 42243 TGGGAGGCGGAGGCGGCTGCTCAAGGTTCAGAGTGGTGGAGACAGCTGACCAACATGG 42184  
QY 4917 TGAAACCCGCTCTTAAAAAATACAAAAATAGCTGGTCACAGTCATGCGCACCTGTAGT 4976  
Db 42183 TGAAACCCGCTCTTAAAAAATACAAAAATAGCTGGTCACAGTCATGCGCACCTGTAGT 42124  
QY 4977 CCCAGCTAATTTGGAAGGCTGAGGC 5000  
Db 42123 CCCAGCTAATTTGGAAGGCTGAGGC 42100

RESULT 14  
ABV93934  
ID ABV93934 standard; DNA; 5982 BP.  
XX AC ABV93934;  
XX 08-JAN-2003 (first entry)  
XX Human colon specific nucleic acid, SEQ ID 25.  
XX Human; colon; cytostatic; vaccine; gene therapy; colon cancer;  
KW colon disorder; metastasis; ds.  
XX Homo sapiens.  
XX WO20027234-A2.  
XX 03-OCT-2002.  
XX 31-OCT-2001; 2001WO-US048414.  
XX 31-OCT-2000; 2000US-0244759P.

XX (DIAD-) DIADEXUS INC.  
XX Sun Y, Recipon H, Ghosh MG, Liu C;  
XX WPI; 2003-018928/01.  
XX New isolated colon-specific nucleic acid molecule, useful for treating  
PT colon cancer, and diagnosing or monitoring the presence of metastases of  
PT colon cancer in a patient.  
XX Claim 1; Page 155-156; 216pp; English.  
XX The present invention relates to human colon specific nucleic acids  
CC (ABV93910-ABV94009) and proteins (ABP68360-ABP68435). The nucleic acids  
CC and proteins are useful for treating colon cancer and colon disorders,  
CC and diagnosing or monitoring the presence of colon disorders and  
CC metastases of colon cancer in a patient  
XX Sequence 5982 BP; 1659 A; 1247 C; 1518 G; 1556 T; 0 U; 2 Other;  
QY Query Match 92.2%; Score 4607.8; DB 8; Length 5982;  
Db Best Local Similarity 99.7%; Pred. No. 0;  
Matches 4628; Conservative 0; Mismatches 12; Indels 3; Gaps 1;  
QY 361 ATGGGCGCGCAGCAGCGCGCGCTTCTCTCTGATGCTTTTGCAGACCGCGGTCTGTG 420  
Db 1 ATGGGCGCGCAGCAGCGCGCGCTTCTCTCTGATGCTTTTGCAGACCGCGGTCTGTG 60  
QY 421 CAGGGGCGCTTGTCTGCTGAGTCCGAGGGCTGCGGCGAACTAGGGGCGCGCGGGGTG 480  
Db 61 CAGGGGCGCTTGTCTGCTGAGTCCGAGGGCTGCGGCGAACTAGGGGCGCGCGGGGTG 120  
QY 481 GAAAAATCGAAATAGCTTTTCTTGGCTTGGAGTTTGTCTAACTTTTGAGAGCACTGC 540  
Db 121 GAAAAATCGAAATAGCTTTTCTTGGCTTGGAGTTTGTCTAACTTTTGAGAGCACTGC 180  
QY 541 TCAACCTATCCGCAAGCCCTCTCCCTACTTTCTGGCTCCAGACCCCGTGAGGAGTGC 600  
Db 181 TCAACCTATCCGCAAGCCCTCTCCCTACTTTCTGGCTCCAGACCCCGTGAGGAGTGC 240  
QY 601 CTACACTGAACTCAGATAGGGGTCTCTCCGCCAGGACCTGCCCTCCCGCGGTGT 660  
Db 241 CTACACTGAACTCAGATAGGGGTCTCTCCGCCAGGACCTGCCCTCCCGCGGTGT 300  
QY 661 CCCGCTCTCGGAGTGAATTTTGGAAACCGCCACTTCCCTTCCCGCAACTAGAAATGCTTT 720  
Db 301 CCCGCTCTCGGAGTGAATTTTGGAAACCGCCACTTCCCTTCCCGCAACTAGAAATGCTTT 360  
QY 721 TAAATAATCTCTAGTTCTCTCACTGAGCTGAGCTAGCCTGGGCTCTTGACCTGG 780  
Db 361 TAAATAATCTCTAGTTCTCTCACTGAGCTGAGCTAGCCTGGGCTCTTGACCTGG 420  
QY 781 AACTCGGGTTTATTTTCCAAATGTGAGTGTGAGTTTTCCTCCAGTCACTCTCCAAACAGG 840  
Db 421 AACTCGGGTTTATTTTCCAAATGTGAGTGTGAGTTTTCCTCCAGTCACTCTCCAAACAGG 480  
QY 841 AAGTTCTTCTCTAGTGTCTTCCGAGAGGCTGAGCAAAACCAACAGAGGATCCGACGG 900  
Db 481 AAGTTCTTCTCTAGTGTCTTCCGAGAGGCTGAGCAAAACCAACAGAGGATCCGACGG 540  
QY 901 GGTTCACCTCAGAACGAATCGTGGCGGTGGGCGCGGAAGAGTGGCGTTGGGGA 960  
Db 541 GGTTCACCTCAGAACGAATCGTGGCGGTGGGCGCGGAAGAGTGGCGTTGGGGA 600  
QY 961 TCTGAATTTCTTCAACATTTCCACCTTTTGGTGGAGCTCTGGGTGGAGGTCTCTAGGGT 1020  
Db 601 TCTGAATTTCTTCAACATTTCCACCTTTTGGTGGAGCTCTGGGTGGAGGTCTCTAGGGT 660  
QY 1021 GGGAGGCTCTTGAGAGAGGCTTACTCTGGGCTTTTCCCACTCTTGGCAATTTGTTCTTTT 1080  
Db 661 GGGAGGCTCTTGAGAGAGGCTTACTCTGGGCTTTTCCCACTCTTGGCAATTTGTTCTTTT 720







Db 2881 ATAGTCCAGGTTTTCAGGAGGCTTAGGTAGGAGAAATCCCTTGAACCCAGGAGGTGCAGG 2940  
Qy 3301 TTGCGAGTGAAGCTGAGATTGTGCCACTGCACTCCAGCGTGGGTGATAGAGTGAAGCTCTGT 3360  
Db 2941 TTGCGAGTGAAGCTGAGATTGTGCCACTGCACTCCAGCGTGGGTGATAGAGTGAAGCTCTGT 3000  
Qy 3361 CTCAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAA 3420  
Db 3001 CTCAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAAAMAAAAA 3060  
Qy 3421 TCTAAATTTGCCCTGAGCAACCAACTCCTGAGTTCAACTACCTAGCTAGACACACCTTAAC 3480  
Db 3061 TCTAAATTTGCCCTGAGCAACCAACTCCTGAGTTCAACTACCTAGCTAGACACACCTTAAC 3120  
Qy 3481 ATTTTCTAGAAATCCACAGCTTTTAGTGGAGTCTGTCTAATCATAGTATTTGGAATAGGAT 3540  
Db 3121 ATTTTCTAGAAATCCACAGCTTTTAGTGGAGTCTGTCTAATCATAGTATTTGGAATAGGAT 3180  
Qy 3541 CTGGGGGCGAGTCAGGGGGTGGCAGCCAGCTGTGGCAGAGAAAGCACACAGGAAAGAGC 3600  
Db 3181 CTGGGGGCGAGTCAGGGGGTGGCAGCCAGCTGTGGCAGAGAAAGCACACAGGAAAGAGC 3240  
Qy 3601 ACCCAGGAGCTGTCAATATGGAAGAAAGACAGAGACTGCAACTCACCCTTCAAAAAATGAGGA 3660  
Db 3241 ACCCAGGAGCTGTCAATATGGAAGAAAGACAGAGACTGCAACTCACCCTTCAAAAAATGAGGA 3300  
Qy 3661 CCAGACACAGCTGATGGTATGAGTTGATGACAGGTGTGGAGCCTCAACATCCTGCTCCC 3720  
Db 3301 CCAGACACAGCTGATGGTATGAGTTGATGACAGGTGTGGAGCCTCAACATCCTGCTCCC 3360  
Qy 3721 CTCCTACTACACATGTTTAAGGCTGTGTCTGTCTCCAGGTTCAACTCTCTGCACTA 3780  
Db 3361 CTCCTACTACACATGTTTAAGGCTGTGTCTGTCTCCAGGTTCAACTCTCTGCACTA 3420  
Qy 3781 CCTCTTCATGGTGGCTCAGACAGGACCTTGGTCTTTCTTTTGAAGCTTTGGGCTA 3840  
Db 3421 CCTCTTCATGGTGGCTCAGACAGGACCTTGGTCTTTCTTTTGAAGCTTTGGGCTA 3480  
Qy 3841 CGTGATGACAGCTGTTCGTGTTCTATGATCATGAGAGTCGCCGTGTGGAGCCCGGAAC 3900  
Db 3481 CGTGATGACAGCTGTTCGTGTTCTATGATCATGAGAGTCGCCGTGTGGAGCCCGGAAC 3540  
Qy 3901 TCCATGGGTTTCCAGTATGAAATTTCAAGCCAGATGTGGCTGCAAGTGTGAGTCTGAA 3960  
Db 3541 TCCATGGGTTTCCAGTATGAAATTTCAAGCCAGATGTGGCTGCAAGTGTGAGTCTGAA 3600  
Qy 3961 AGGGTGGATCATATGTTCACTGTTGACTTTGGAATTTGGAATTTGGAATTTGGAATTTGGAATTTGGA 4020  
Db 3601 AGGGTGGATCATATGTTCACTGTTGACTTTGGAATTTGGAATTTGGAATTTGGAATTTGGAATTTGGA 3660  
Qy 4021 CAAGGGTATGGAGAGGGGGCTCACCTTCTGAGGTTGTGAGAGCTTTTCACTCTTTTC 4080  
Db 3661 CAAGGGTATGGAGAGGGGGCTCACCTTCTGAGGTTGTGAGAGCTTTTCACTCTTTTC 3720  
Qy 4081 ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGCTTGTGGAGCTATATGGAATTTCAACACCAAC 4140  
Db 3721 ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGCTTGTGGAGCTATATGGAATTTCAACACCAAC 3780  
Qy 4141 GAAATTTGCTTCTGAGATCATTTGGTCTTGGGATGGTGGAAATAGGAGACCTATTCCTT 4200  
Db 3781 GAAATTTGCTTCTGAGATCATTTGGTCTTGGGATGGTGGAAATAGGAGACCTATTCCTT 3840  
Qy 4201 TGGTTGCGAGTTAAACAGGCTGGGGAATTTTTCAGAGTCCACACCTCGAGGTCACTCTG 4260  
Db 3841 TGGTTGCGAGTTAAACAGGCTGGGGAATTTTTCAGAGTCCACACCTCGAGGTCACTCTG 3900  
Qy 4261 GGCTGTGAAATGCAAGAGACAAACAGTACCGAGGCTACTGGAAGTATCGGTATGATGG 4320  
Db 3901 GGCTGTGAAATGCAAGAGACAAACAGTACCGAGGCTACTGGAAGTATCGGTATGATGG 3960  
Qy 4321 CAGGACCACTTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGAGAACCCAGGGCC 4380  
Db 3961 CAGGACCACTTTGAATTTCTGCCCTGACACACTGGATTGGAGAGCAGAGAACCCAGGGCC 4020

Qy 4381 TGGCCCAACAAGCTGGAGTGGGAAAGGCACAAGATTCGGGCCAGGCAGAACAGGGCCTAC 4440  
Db 4021 TGGCCCAACAAGCTGGAGTGGGAAAGGCACAAGATTCGGGCCAGGCAGAACAGGGCCTAC 4080  
Qy 4441 CTGAGAGGGGACTGCCCTGCAAGCTGCAGAGTTCGTGGAGCTGGGAGAGGTGTTTG 4500  
Db 4081 CTGAGAGGGGACTGCCCTGCAAGCTGCAGAGTTCGTGGAGCTGGGAGAGGTGTTTG 4140  
Qy 4501 GACCAACAAGGATAGGTGGAAACACACTTCTGCCCTATATCTCTAGTGGCAGAGTGGAGG 4560  
Db 4141 GACCAACAAGGATAGGTGGAAACACACTTCTGCCCTATATCTCTAGTGGCAGAGTGGAGG 4200  
Qy 4561 AGGTTGCAGGCGACCGAATCCCTGGTGGAGTTCAGAGGTGGCTGAGGCTGTGTGCCCTC 4620  
Db 4201 AGGTTGCAGGCGACCGAATCCCTGGTGGAGTTCAGAGGTGGCTGAGGCTGTGTGCCCTC 4260  
Qy 4621 TCCAAATTTCTGGGAAGGACTTCTCAATCCTAGAGTCTCTACCTTATAATTTGAGATGTA 4680  
Db 4261 TCCAAATTTCTGGGAAGGACTTCTCAATCCTAGAGTCTCTACCTTATAATTTGAGATGTA 4320  
Qy 4681 TGAGACAGCCACAAGTCAATGGGTTTAAATTTCTTTTCTCCATGCAATATGGCTCAAGGGAA 4740  
Db 4321 TGAGACAGCCACAAGTCAATGGGTTTAAATTTCTTTTCTCCATGCAATATGGCTCAAGGGAA 4380  
Qy 4741 GTGTCTATGGCCCTTGTCTTTTATTAACCAATATCTTTTGTATATTTATACCTGTTAA 4800  
Db 4381 GTGTCTATGGCCCTTGTCTTTTATTAACCAATATCTTTTGTATATTTATACCTGTTAA 4440  
Qy 4801 AAATTCAGAAATGTCAAGCGGGGACCGGTGGCTCACCCCTGTAATCCAGCACCTTTGGG 4860  
Db 4441 AAATTCAGAAATGTCAAGCGGGGACCGGTGGCTCACCCCTGTAATCCAGCACCTTTGGG 4500  
Qy 4861 AGGCGAGGCGGGTGG---TCACAAGTTCAGAGTTTGAGACCGCTTGACCAACATGGT 4917  
Db 4501 AGGCGAGGCGGACAGATCACCTGAGTTCAGAGTTTGAGACCGCTTGACCAACATGGT 4560  
Qy 4918 GAAACCCGCTCTCAAAAAAATACAAAAATTTAGCTGCTCACAGTCAATGCGCACCTGTACTC 4977  
Db 4561 GAAACCCGCTCTCAAAAAAATACAAAAATTTAGCTGCTCACAGTCAATGCGCACCTGTACTC 4620  
Qy 4978 CCAGCTAATTTGGAAGGCTGAGGC 5000  
Db 4621 CCAGCTACTCGGAGGCTGAGGC 4643

RESULT 15  
ABL34142

ID ABL34142 standard; DNA; 8622 BP.

XX ABL34142;

XX 26-MAR-2002 (first entry)

XX Human immune system associated gene SEQ ID NO: 2115.

XX Human; immune system disease; cytosine methylation; antiasthmatic;  
KW antiarteriosclerotic; antianaemic; cytosatic; nootropic;  
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
KW antineuritic; antiarthritic; antidiabetic; antipsoriatic;  
KW antineuritic; cancer; eye disease; arteriosclerosis; anaemia;  
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;  
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;  
ds.

OS Homo sapiens.

XX WO200200928-A2.

XX 03-JAN-2002.

XX 02-JUL-2001; 2001WO-EP007537.



PR	30-JUN-2000; 2000DE-01032529.
XX	01-SEP-2000; 2000DE-01043826.
XX	(EPIG-) EPIGENOMICS AG.
PA	Olek A, Piepenbrock C, Berlin K;
PI	WFI; 2002-130909/17.
XX	
DR	Nucleic acid comprising fragment of chemically modified gene, useful for
XX	diagnosis and treatment of diseases associated with abnormal cytosine
PT	methylation.
PT	
XX	
PS	Claim 1; SEQ ID NO 2115; 32pp + Sequence Listing; German.
XX	
CC	The present invention provides a number of human immune system associated
CC	genes which are modified by the methylation of cytosines. The sequences
CC	can be used in the diagnosis and treatment of immune system disorders,
CC	including eye diseases such as retinopathy, neovascular glaucoma and
CC	macular degeneration, arteriosclerosis, anemia, cancer, acute myeloid
CC	leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC	rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC	diseases. The present sequence is a gene of the invention
XX	
SQ	Sequence 8622 BP; 2410 A; 100 C; 2013 G; 4099 T; 0 U; 0 Other;
	Query Match 51.1%; Score 2556.4; DB 6; Length 8622;
	Best Local Similarity 80.1%; Pred. No. 0;
	Matches 3015; Conservative 0; Mismatches 746; Indels 1; Gaps 1;
QY	1 TCTAAGGTTGAGATAAAATTTTTTAAATGTATGATTGAATTTTGAAAATCATAAATATTTA 60
DB	4862 TTTAAGGTTGAGATAAAATTTTTTAAATGTATGATTGAATTTTGAAAATTTAAATATTTA 4921
QY	61 AATATCTAAAGTTCAGATCAGAATTCGGAAGCTACTTCCCCCAATCAACACCCT 120
DB	4922 AATATTTAAAGTTTAGATTAGATTTGCGAAGTATTTTTTTTAAATAATAATATTTT 4981
QY	121 TCAGGATTTAAAAACCAAGGGGCACCTGGATCACCTAGTGTCTTTCACAAGCAGGTACCTT 180
DB	4982 TTAGGATTTAAAAATTAAGGGGATATTGGATTTATTAGTGTCTTTATAAGTAGGTATTTT 5041
QY	181 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTGTCTTTTACCAGGAAGTT 240
DB	5042 TTGTGTGTAGGAGAGAGAAATTAAGATTTTGAAGATTTGTGTGTCTTTATTAGGAAGTT 5101
QY	241 TTACTGGGCATCTCTGAGCCTAGGCCATAGCTGTAGGTTGACTTCTGGAGCCATCCCCT 300
DB	5102 TTATPVGGTATTTTTTCAGTTTAGTGAATAGTTGTAGGGTGATTTTTTGGAGTTATTTTCG 5161
QY	301 TTTTCCCGCCCCCAAAGAACGGAGATTTAACGGGACGTGCGGCCACAGAGCTGGGGAA 360
DB	5162 TTTTTCGTCTTTTAAAGAACGGAGATTTAACGGGACGTGCGGTTAGAGTTGGGGAA 5221
QY	361 ATGGCCCCCGAGCAGCCCGCGCTTCTCCTCTGATGCTTTTTCAGACCGCGGTCTCTG 420
DB	5222 ATGGGTCGCGAGTTAGTCTCGCGCTTTTTTTTTTTTGTATGTTTTTGTAGATCGCGGTTTG 5281
QY	421 CAGGGCGCTTGCTGCGTGAGTCGAGGCGCTCGGGCGAATAGGGCGCGCGCGGGGTG 480
DB	5282 TAGGGCGCTTGTTCGCTGAGTTCGAGGGTTGCGGGCGAATTAGGGCGCGCGCGGGGTG 5341
QY	481 GAAAAATCGAAACTAGCTTTTCTTCGCTTGGGAGTTTGCTAACTTTGGAGGACCTGC 540
DB	5342 GAAAAATCGAAATAGTTTTTTTTTTTCGCTTTGGAGTTTGTTAAATTTTGAGGATTTGT 5401
QY	541 TCAACCTATCCGAAGCCCTCTCCCTACTTCTTCGCTCCAGACCCCGTAGGGAGTGC 600
DB	5402 TTAATTTTATTCGTAAGTTTTTTTTTTTTTATTTTTTTCGTTTAGATTTTCGTGAGGAGTGT 5461
QY	601 CTACCACTGAATCGAGATAGGGGTCCCTCGCCCCCAGACCTGCCCCCTCCCGCGCTGT 660
DB	5462 TTATATTGAATTCGATAGGGGTCTTTTCGTTTAGGATTTGTTTTTTTTTTTTTTTCGTTGT 5521



QY 1741 CAGGGAGAGACAGGAAACAGTCTTTACCTTTTGATATTTTCATCTTAGTGGGAGA 1800  
 DB 6602 TAAGGGAGAGAGTAGGGAATAAGTTTATTTTGTATATTTTGTATTTTGTATTTTAGTGGGAGA 6661  
 QY 1801 GATGACAAATAGCAAAATAGCAGAAAGATATACACATCAGGAAATCATGGGTGTGTGA 1860  
 DB 6662 GATGATATAGTAATAGTAGTAAGAGATATATATATATAGGAATATGGGTGTGTGA 6721  
 QY 1861 GAAGCAGAGAACTCAGGGCAAGTCACTCTGGGGCTGACACTTTGACGAGACATGAAGGA 1920  
 DB 6722 GAAGTAGAGAACTTAGGGTAAAGTTATTTTGGGGTTGATATTTGAGTAGAGATATGAAGGA 6781  
 QY 1921 AATAGAAATGATTTGACTGGGAGCAGTATTTCCAGGCAAACTCAGTGGGCTGGCAAG 1980  
 DB 6782 AATAGAAATGATTTGATTTGGGAGTAGTATTTTATAGGTAAATCAGTGGGTTCGGTAAG 6841  
 QY 1981 TTGGATTTAAAGACGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGTGGGGGGGGGG 2040  
 DB 6842 TTGGATTTAAAGACGGGTTTTTATAGTATTTATTTATGTGTGTGTGTGGGGGGGGGG 6901  
 QY 2041 CGGCGTGGGGTGGGAAGGGGACTTACCATCTGCATGTAGTAGTCTTAGCAGTATCCTGT 2100  
 DB 6902 CGGCGTGGGGTGGGAAGGGGATTTATTTGTATGTAGGATGTTTAGTAGTATTTTGT 6961  
 QY 2101 CCTCCCTACTACTAGTGTCTTAGGAGGACTCCCCAGTCTTCACAAACAAATGCTCT 2160  
 DB 6962 TTTTATTTATTTATAGGTGTAGGAGTATTTTATAGTTTGTATTAATTAATAATGTTTT 7021  
 QY 2161 AAATCTTGGCACATGCTCACTAGTAGACAACTCCTGGTTAAGAAAGCTCGGGTTCAAAAA 2220  
 DB 7022 AAATCTTGTATATGTTATTTAGTAGATATAATTTTGGTTAAGAAAGTTCGGGTGAAAA 7081  
 QY 2221 AATAAACAGTAGTGTCTGGGAGTAGAGCCCAAGAAAGTAGTAAATGGGCTCAGAAAGGA 2280  
 DB 7082 AATAAATAGTAGTGTGGGAGTAGAGGTTAAGAAAGTAGTAAATGGGTTTAGAAGAGA 7141  
 QY 2281 GCCAACAACAGGTTGTGCAGGCGCTGTAGGCTGTGGTGTGAATCTTAGCCCAAGGATA 2340  
 DB 7142 GTTATAAATAGGTTGTGTAGGCGTTTGTAGGTTGTGGTGTGAATTTTAGTTAAGGATA 7201  
 QY 2341 ACAGTGTCTGTGCACAGGCTTTTAAAGANTCTCTGGCTGTATGTGGAAAGCAGAAATG 2400  
 DB 7202 ATAGTGTATTTGTATAGGTTTTTAAAGANTCTTTTGGTTGTATGTGGAAAGTAGAATG 7261  
 QY 2401 AAGGAGCAACAGTAAAGCAGGAGCCAGCCAGGAGCTGTACAGTCCAGGCAAG 2460  
 DB 7262 AAGGAGTAAATAGTAAAGTAGGAGTTTAGTTAGGAAGTTCTATATAGTTTAGGTAAG 7321  
 QY 2461 AGGTAGTGGAGTGGGCTGGGTGGGACAGAAAGGAGTGACAAACCATTTCTCTCTGNA 2520  
 DB 7322 AGGTAGTGGAGTGGGTGGGTGGGAAATAGAAAGGAGTGATAAATTTATTTTGGAA 7381  
 QY 2521 TATATTTCAAGGAAGTTCTCAAGGATTTCTATTTGTGTGAGAAAGAGAAATTTGG 2580  
 DB 7382 TATATTTCAAGGAAGTTCTCAAGGATTTCTATTTGTGTGAGAAAGAGAAATTTGG 7441  
 QY 2581 CTGGGTGTAGTACTCATCCCAAGGAGGAGCCAGGAGAGCAGATTCCTGAGCTCAGA 2640  
 DB 7442 TTGGGTGTAGTATTTATGTTAAGGAGGAGTTAAGGAGAGTAGATTTTGTAGTTTAGGA 7501  
 QY 2641 GTTCAAGACCAGCTGGGCAACACAGCAAAACCCCTTCTCTACAAAATACAAAATTA 2700  
 DB 7502 GTTAAAGATTTAGTTTGGGTAAATAGTAAAAATTTTTTTTTTATAAAAAATATAAAAAATTA 7561  
 QY 2701 GCTGGGTGTGGTGGCATGCCTGTGATCTAGCTACTCGGAGGCTGAGGTGGAGGTA 2760  
 DB 7562 GTTGGGTGTGGTGGTATGTATTTGTGATTTTATTTAGTTTATTCGGGAGGTTGAGGTGGAGGTA 7621  
 QY 2761 TTGCTTGACCCAGGAGTTGAGGCTGAGTGCAGTGCAGCAATGATGTGCCACTGTACTTCAGC 2820  
 DB 7622 TTGTTTGAGTTTAGGAAGTTGAGGTTGTAGTGAGTATGATTTGTGTATTTAGT 7681  
 QY 2821 CTAGGTGACAGCAAGACCCCTGTCTCCCTGACCCCTGAAAAAGAGAGATTAAGT 2880

DB 7682 TAGGTGATAGTAGATTTTTTGTATTTTTTGAATTTTTTGAATAAGAGATTAAGT 7741  
 QY 2881 TGACTTTTCTTTTATTTTAAATTTTATTTGGCTCAGCAGTGGGTAAATTTGCAATGCCAT 2940  
 DB 7742 TGAATTTGTTTTTATTTTAAATTTTATTTGTTTTCAGTAGTGGGTAAATTTGGTAAATGTTAT 7801  
 QY 2941 TTCTGAGATGTGAAGGAGAGAGAGAGAGTGTGGGTAAATCAAGGATCTGCATTTG 3000  
 DB 7802 TTTTGAGATGCTGAAGGTAGAGAAAGAGTAGTTTGGGTAAATTAAGGATTTGTTATTT- 7860  
 QY 3001 GGACATGTTAAGTTTTCAGATTTCCAGTCCAGGCTTCCAAGTGTGAGGCCACATAGGCAGTT 3060  
 DB 7861 GGAATGTTAAGTTTTCAGATTTTATTTAGTTTATTTAGTGTGAGGTATATATAGTAGTT 7920  
 QY 3061 CAGTGAAGAAATTCAGGACCAAGGCTGGGCAAGGTCGGCTCACTTCTGTPAATCCCAAGCACT 3120  
 DB 7921 TAGTGAAGAAATTTAGGATTTAAGGTTGGGTACGGTGGTTATTTTGTAAATTTTAGTATT 7980  
 QY 3121 TTGGTGGCTGAGGAGAGGTAGATCATTTTCAGGTTCAGGAGTTTTCAGACAAAGCTTGGCCACA 3180  
 DB 7981 TTGGTGGTTCAGGTAGGTAGATTTATTTGAGGTTCAGGAGTTTTCAGATAAGTTTGGTAAATA 8040  
 QY 3181 TGGTGAACCCCATGCTCTACTAAAAATACAAAAATTTAGCCTGGTGTGGTGGCAGCGCT 3240  
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 DB 8161 TTGTAGTGCAGTGCAGTTTGTCTTATTTAGTTTGGTGTAGTGCAGTGCAGTCTGT 8220  
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 DB 8581 TTTTATTTATATATAGGTTTAAAGGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8622



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2005, 09:06:57 ; Search time 15746.3 Seconds  
(without alignments)  
12086.738 Million cell updates/sec

Title: US-09-497-957-1\_COPY\_1\_5000  
Perfect score: 5000  
Sequence: 1 TCTAAGTTCAGATAAAATT.....GCTAATTGGAAGCTGAGGC 5000

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

- 1: gb\_est1.\*
- 2: gb\_est2.\*
- 3: gb\_est3.\*
- 4: gb\_est4.\*
- 5: gb\_est5.\*
- 6: gb\_est6.\*
- 7: gb\_est7.\*
- 8: gb\_gses1.\*
- 9: gb\_gses2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	612.8	12.3	691	4	BG926549 HNC42-1-G
C 2	589	11.8	648	9	AG116246 Pan trogl
C 3	464.2	9.3	531	8	AQ703007 HS_5443_B
C 4	420.8	8.4	442	2	AW449998 UI-H-BI3-
C 5	412.6	8.3	533	8	AQ790990 HS_2239_B
C 6	408.4	8.2	443	8	AQ111002 CIT-HSP-2
C 7	313.4	6.3	326	8	AQ056874 CIT-HSP-2
C 8	298	6.0	603	7	CN264281 170005313
C 9	293	5.9	420	8	AQ296898 HS_3005_B
C 10	281.6	5.6	3713	3	BC041839 Homo sapi
C 11	277.4	5.5	6146	8	AQ839831 260L13-C4
C 12	268.8	5.4	793	4	BM551225 AGENCOURT
C 13	267.2	5.3	5940	3	CR627133 Homo sapi
C 14	266.2	5.3	972	5	BQ712091 AGENCOURT
C 15	266	5.3	570	2	BE272926 601171213
C 16	265	5.3	819	4	BG747345 602704818
C 17	264	5.3	544	4	BM751283 K-EST0027
C 18	264	5.3	560	1	AU279987 AU279987
C 19	264	5.3	3288	3	HSMB02613
C 20	262.4	5.2	535	6	CB162561 K-EST0223
C 21	259.4	5.2	6056	3	CR627178 Homo sapi
C 22	258.4	5.2	2009	3	HSMB02716
C 23	258.2	5.2	714	6	CD366358 UI-H-FTL1
C 24	256	5.1	4975	8	AQ839811 260L13-C4

C 25	254.6	5.1	546	2	BE809138
C 26	253	5.1	828	5	BX457226
C 27	252.8	5.1	4207	3	BC034315 Homo sapi
C 28	251.8	5.0	761	5	BQ707017 AGENCOURT
C 29	250.8	5.0	1723	3	BC039095
C 30	247.6	5.0	741	7	CR748096
C 31	245.8	4.9	6789	3	HSMB07629
C 32	245.2	4.9	1374	3	BC017002
C 33	242.4	4.8	4750	3	HSMB04795
C 34	242.2	4.8	2455	3	AF461900
C 35	242	4.8	724	6	CA427092
C 36	240	4.8	388	2	AW069227
C 37	239	4.8	2531	3	BC020559
C 38	238.6	4.8	731	7	CN307840
C 39	238.6	4.8	734	5	BQ707295
C 40	238	4.8	3863	3	BC035034
C 41	237.4	4.7	624	1	AA601356
C 42	237.2	4.7	1300	8	AF057104
C 43	237	4.7	735	7	CF146929
C 44	236.8	4.7	839	8	AQ900274
C 45	236.6	4.7	647	4	BM559057

ALIGNMENTS

RESULT 1  
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LOCUS HNC42-1-G8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA linear EST 06-NOV-2001  
DEFINITION sequence.  
ACCESSION BG926549  
VERSION BG926549.1 GI:14321072  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 691)  
AUTHORS Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J., Sathe, G., Mul, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and Lark, M.W.  
TITLE Identification and initial characterization of 5000 expressed sequence tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries  
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
MEDLINE 21482651  
PUBMED 11597177  
COMMENT Contact: Sanjay Kumar  
UW2109  
GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: sanjay.kumar@gsk.com  
Seq primer: T7  
FEATURES  
Location/Qualifiers  
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Matches 617; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
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QY 1457 GTGGGTACACAGCGCGGCTCAGCAGCAGCACTTTGAGTTTTGGTACTACGTGTATCCACAT 1516  
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QY 1757 GAAACAAGTCTTTACCTTTGATATTTTGCATTTCTAGTGGGAGAGATGACAATAAGCABA 1816  
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QY 1877 GCGAAGTCACTCTGGGGCTGACCTTGAGCAGAGACATGAGAGAAATAAGATGATATTG 1936  
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QY 1937 ACTGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTCGCAAGTTGGATTAAAGCGG 1996  
Db 151 ACTGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTCGCAAGTTGGATTAAAGCGG 92  
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Db 91 GTTTTCTCAGCGGACGCGTGGGT 68

RESULT 2  
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LOCUS Pan troglodytes DNA, clone: PTB-123L15.R, genomic survey sequence.  
DEFINITION  
ACCESSION AG116246  
VERSION AG116246.1 GI:16736765  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
1  
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
BAC end sequences of Library PTB  
Unpublished  
2 (bases 1 to 648)  
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
Direct Submission  
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail:chimpses@gsc.riken.go.jp; URL:http://hgp.gsc.riken.go.jp/;  
Tel:81-45-503-9111, Fax:81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.  
PRIMERS

Sequencing: M13Rev  
LIBRARY Vector : pKS145  
R.Site 1 : SacI  
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Location/Qualifiers  
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Best Local Similarity 99.2%; Pred. No. 4.4e-80;  
Matches 592; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
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QY 1186 TCTCAAAAGTACTGATAATGAACATGTAAGCAATGCATCACTTCTAAGTTACATTCATA 1245  
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DEFINITION genomic clone Plate=1019 Col=17 Row=N, genomic survey sequence.  
ACCESSION AQ03007  
VERSION AQ03007.1 GI:5412433  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.



REFERENCE 1 (bases 1 to 531)  
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.  
 TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
 PUBMED 99380589  
 COMMENT 10449764  
 Contact: Mahairas G, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering\_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu  
 Plate: 1019 row: N column: 17  
 Seq primer: T7  
 Class: BAC ends  
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 Query Match 9.3%; Score 464.2; DB 8; Length 531;  
 Best Local Similarity 96.5%; Pred. No. 5.2e-61;  
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 DB 42 ACACGATTTGGAGCAGCAGACACCCAGGCGCTGGCCACCAAGCTGGAGTGGATG 101  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 442)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapsb@mail.nih.gov  
 The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: www-bio.lnl.gov/bbrp/image/image.html  
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 POLYA=Yes.  
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driver population). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806. TAG\_TISSUE=colon  
TAG\_LIB=NCI CGAP\_Col0  
TAG\_SEQ=AAACG"

## ORIGIN

Query Match 8.4%; Score 420.8; DB 2; Length 442;  
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Matches 422; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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QY 385 CTTCTCCTCTGATGCTTTTGCAGACCGCGGTCTGCAGGGGGCTTGTGCGTGAGTCC 444  
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QY 445 GAGGGCTGGCGGGAATAAGGGCGCGGGGGTGGAAAAATCGAAACTAGCTTTTCT 504  
Db 320 GAGGGCTGGCGGGAATAAGGGCGCGGGGGTGGAAAAATCGAAACTAGCTTTTCT 261  
QY 505 TTGCGCTTGGGAGTTGCTAACTTTTGAGAGACCTGCTCAACCTATCCGAGCCCTCT 564  
Db 260 TTGCGCTTGGGAGTTGCTAACTTTTGAGAGACCTGCTCAACCTATCCGAGCCCTCT 201  
QY 565 CCCTACTTTCTGGTCCAGACCCGCTGAGGAGTGCTACCACTGAACTGCAGATAGGG 624  
Db 200 CCCTACTTTCTGGTCCAGACCCGCTGAGGAGTGCTACCACTGAACTGCAGATAGGG 141  
QY 625 TCCTCGCCCCAGGACCTGCCCTCCCGCGCTGTCGGGCTCTCGGAGTGACTTTTG 684  
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QY 685 GAACCGCCACTCCCTCCCGCACTAGATGCTTTTAAATAATCTCGTAGTTCCTCAC 744  
Db 80 GAACCGCCACTCCCTCCCGCACTAGATGCTTTTAAATAATCTCGTAGTTCCTCAC 21  
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Db 20 TTCA 17

## RESULT 5

AQ790990/c  
LOCUS  
DEFINITION HS 2239\_B1\_D04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2239 Col=7 Row=H, genomic survey sequence.

ACCESSION AQ790990

VERSION AQ790990.1 GI:5698614

KEYWORDS GSS.

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

MEDLINE 95380589

PUBMED 1049764

## COMMENT

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones may be purchased from Research Genetics (info@resgen.com).  
BAC end Web Server: http://www.htsc.washington.edu  
Plate: 2239 row: H column: 7  
Seq primer: M13 Reverse  
Class: BAC ends  
High quality sequence stop: 533.

## FEATURES

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Best Local Similarity 91.6%; Pred. No. 3.9e-53;  
Matches 447; Conservative 0; Mismatches 40; Indels 1; Gaps 1;  
QY 2685 AAAAAACAAAAAATAGCTGGGTGGTCATGCACCTGTGATCCTAGCTACTCGGGAG 2744  
Db 533 AAAAAACAAAAAATAGCTGGGTGGTCATGCACCTGTGATCCTAGCTACTCGGGAG 474  
QY 2745 GCTGAGGTGGGGGTATTGCTTTGAGCCCAAGGTTGAGGCTGCAGTGAGCCATGCTGT 2804  
Db 473 CTGAGGTGGAGGGTATTGCTTTGAGCCCAAGGTTGAGGCTGCAGTGAGCCATGCTGT 414  
QY 2805 GCCACTGTACTTCAGCTAGGTGACAGCAGACAGACCTGTCTCCCTGACCCCTGAAAA 2864  
Db 413 GCCACTGTATTCAAGCTAGGTGACAGCAGCAGACCTGTCTCCCTGACCCCTGAAAA 354  
QY 2865 ACAGAGAGCTTAAAGTTGACTTTGTTTATTATTTTATTTTATTTGSCCTGAGCAGTGGG 2924  
Db 353 ACAGAGAGCTTAAAGTTGACTTTGTTTATTATTTTATTTTATTTGSCCTGAGCAGTGGG 294  
QY 2925 TAATTGGCAATGCCATTTCTGAGATGGTGAAGCGAGAGGAAAGAGCAGTTTGGGGTAAAT 2984  
Db 293 TAATTGGCAATGCCATTTCTGAGATGGTGAAGCGAGAGGAAAGAGCAGTTTGGGGTAAAT 234  
QY 2985 CAAGATCTGCATTTGGGACATGTTAAGTTTGAGATTCAGTCAGCTTCCAGTGGTGA 3044  
Db 233 CAAGATCTGCATTT-GGACATGTTAAGTTTGAGATTCAGTCAGCTTCCAGTGGTGA 175  
QY 3045 GGCACATAGGAGTTTCAAGTAAAGAAATTCAGGACCAAGGCTGGGACGCTGCCTCACITT 3104  
Db 174 GGCACATAGGAGTTTCAAGTAAAGAAATTCAGGACCAAGGCTGGGACGCTGCCTCACITT 115  
QY 3105 CTGTAATCCAGCAGCTTTGTTGGTGGTGAAGCAGGTAGATCAATTTAGGTCAGGAGTTTGAG 3164  
Db 114 CTGTAATCCAGCAGCTTAAGGGAGCTGAGGAGGTAGATCAATTTAGGTCAGGAGTTTGAG 55  
QY 3165 ACAGCTT 3172  
Db 54 ACATGCTT 47

## RESULT 6

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DEFINITION AQ111002 CIT-HSP-2370L14.TR CIT-HSP Homo sapiens genomic clone 2370L14, genomic survey sequence.  
ACCESSION AQ111002  
VERSION AQ111002.1 GI:3487692  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.



REFERENCE 1 (bases 1 to 443)  
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,  
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and  
Venter,J.C.  
TITLE Use of a random human BAC End Sequence Database for Sequence-Ready  
Map Building  
JOURNAL Unpublished (1998)  
COMMENT Other GSSs: CIT-HSP-2370L14.TF  
Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: mdadams@tigr.org  
Clones are available from Research Genetics (info@resgen.com). BAC  
end search page:  
http://www.tigr.org/tldb/hungen/bac\_end\_search/bac\_end\_search.html.  
Seq primer: M13 Reverse  
Class: BAC ends.  
FEATURES  
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HindIII"

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Best Local Similarity 99.5%; Pred. No. 1.8e-52;  
Matches 420; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
Db 2752 TGGAGGGTATTGCTTGAGCCCGAGGAAGTTGAGGCTGCAGTCAGCCATGACTGTGCCACTG 2811  
|||  
443 TGAAGGGTATTGCTTGAGCCCGAGGAAGTTGAGGCTGCAGTCAGCCATGACTGTGCCACTG 384  
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2812 TACTTCAGCTAGTGTGACAGCAGACCCCTGTCTCCCTGACCCCTGAAAAAGAGAAG 2871  
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383 TACTTCAGCTAGTGTGACAGCAGACCCCTGTCTCCCTGACCCCTGAAAAAGAGAAG 324  
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2872 AGTTAAAGTTGACTTTCTTTTATTATTTTAAATTTTATTTGCGCTGAGCAGTCGGGTAATTGG 2931  
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323 AGTTAAAGTTGACTTTCTTTTATTATTTTAAATTTTATTTGCGCTGAGCAGTCGGGTAATTGG 264  
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2932 CAATGCCATTTCTGAGATGCTGAAGGCAGAGGAAGCAGATTTGGGGTAAATCAAGGAT 2991  
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263 CAATGCCATTTCTGAGATGCTGAAGGCAGAGGAAGCAGATTTGGGGTAAATCAAGGAT 204  
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2992 CTCGATTTGGGACATGTTAAGTTTGAATTCAGTTCAGGCTTCAAGTGTGTGAGGCCACA 3051  
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203 CTCGATTTT-GGACATGTTAAGTTTGAATTCAGTTCAGGCTTCAAGTGTGTGAGGCCACA 145  
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3052 TAGCGAGTTCAGTGAAGATTCAGGACCAAGCTGGGCAAGCTGCGTCACTTCTGTAT 3111  
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144 TAGCGAGTTCAGTGAAGATTCAGGACCAAGCTGGGCAAGCTGCGTCACTTCTGTAT 85  
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3112 CCCAGCACTTTGGTGGCTGAGGCGAGGTAGATCATTTGAGGTCAGGAGTTTGAGACAAGCT 3171  
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84 CCCAGCACTTTGGTGGCTGAGGCGAGGTAGATCATTTGAGGTCAGGAGTTTGAGACAAGCT 25  
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3172 TG 3173  
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24 TG 23  
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RESULT 7  
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LOCUS 326 bp DNA linear GSS 30-JUL-1998  
AQ056874

DEFINITION CIT-HSP-2339H7.TR CIT-HSP Homo sapiens genomic clone 2339H7,  
genomic survey sequence.  
ACCESSION AQ056874  
VERSION AQ056874.1 GI:3353480  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 326)  
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,  
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,  
Simon,M. and Venter,J.C.  
TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map  
Building (1998)  
JOURNAL Unpublished (1998)  
COMMENT Other GSSs: CIT-HSP-2339H7.TF  
Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: mdadams@tigr.org  
Clones are available from Research Genetics (info@resgen.com). BAC  
end search page:  
http://www.tigr.org/tldb/hungen/bac\_end\_search/bac\_end\_search.html.  
Seq primer: M13 Reverse  
Class: BAC ends.  
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HindIII"

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Best Local Similarity 99.4%; Pred. No. 6.3e-38;  
Matches 325; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
Qy 2839 CCTGTCTCCCTGACCCCTGAAAGAGAGAGTAAAGTTGACCTTGTCTTTATTT 2898  
|||  
326 CCTGTCTCCCTGACCCCTGAAAGAGAGAGTAAAGTTGACATTTCTTTATTT 267  
|||  
2899 TAATTTTATTTGGCTCAGCAGTCGGGTAAATGGCAATGCCATTTCTGAGATGGTGAAGGC 2958  
|||  
266 TAATTTTATTTGGCTCAGCAGTCGGGTAAATGGCAATGCCATTTCTGAGATGGTGAAGGC 207  
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2959 AGAGGAAGAGCAGTTTGGGGTAAATCAAGGATCTGCAATTTGGGACATGTTAAGTTTGAG 3018  
|||  
206 AGAGGAAGAGCAGTTTGGGGTAAATCAAGGATCTGCAATTT-GGACATGTTAAGTTTGAG 148  
|||  
3019 ATTCCAGTCAGGCTTCAAGTGTGTGAGGCCACATAGCAGTTTCAGTGTAGAATTCAGGA 3078  
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147 ATTCCAGTCAGGCTTCAAGTGTGTGAGGCCACATAGCAGTTTCAGTGTAGAATTCAGGA 88  
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3079 CCAAGCTGGGCAAGCTGCTCACTTCTGTAATCCAGCACTTTGGTGGCTGAGGCAAGGT 3138  
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87 CCAAGCTGGGCAAGCTGCTCACTTCTGTAATCCAGCACTTTGGTGGCTGAGGCAAGGT 28  
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3139 AGATCATTTTCAGGTCAGGAGTTTGAGA 3165  
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27 AGATCATTTTCAGGTCAGGAGTTTGAGA 1

RESULT 8  
CN264281



LOCUS CN264281 603 bp mRNA linear EST 16-MAY-2004  
DEFINITION 17000531346032 GRN\_EB Homo sapiens cDNA 5', mRNA sequence.  
ACCESSION CN264281  
VERSION CN264281.1 GI:47280695  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 603)  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
Brandenberger R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,  
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R.,  
Lebkowski, J. and Stanton, L. W.  
TITLE Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation  
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)  
COMMENT Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
Insert Length: 603 Std Error: 0.00.  
Location/Qualifiers  
1. .603  
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derived from H1, H7 and H9 cells"  
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from embryoid body outgrowths derived from hES cell lines  
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free  
conditions."

FEATURES  
source  
Location/Qualifiers  
1. .603

ORIGIN  
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Best Local Similarity 71.2%; Pred. No. 1.2e-35;  
Matches 517; Conservative 0; Mismatches 0; Indels 209; Gaps 1;  
QY 3762 GTTCACACTCTGCACTACCTCTTCATGGTGCCTCAGACGAGACCTTGGTCTTCT 3821  
DB 87 GTTCACACTCTGCACTACCTCTTCATGGTGCCTCAGACGAGACCTTGGTCTTCT 146  
QY 3822 TGTTTGAAGCTTTGGGCTAGTGGATGACGAGTGTTCGTTCTATGATCATGAGATC 3881  
DB 147 TGTTTGAAGCTTTGGGCTAGTGGATGACGAGTGTTCGTTCTATGATCATGAGATC 206  
QY 3882 GCGTGTGGAGCCCGAATCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 3941  
DB 207 GCGTGTGGAGCCCGAATCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGC 266  
QY 3942 AGCTGAGTCAGATCTGAAGGGTGGATCAGATGTTCACTGTGTGACTTCTGACATATTA 4001  
DB 267 AGCTGAGTCAGATCTGAAGGGTGGATCAGATGTTCACTGTGTGACTTCTGACATATTA 326  
QY 4002 TGGAAATACACACACACAGCAGGATATGGAGAGGGGSCCTCACCTTCTCAGGTGTG 4061  
DB 327 TGGAAATACACACACAGCAGGATATGGAGAGGGGSCCTCACCTTCTCAGGTGTG 349  
QY 4062 CAGAGCTTTTTCATCTTTTTCATGTCATCTTGAAGGAACAGCTGGAAGTCTGAGGTCTTGTG 4121  
DB 350 ----- 349  
QY 4122 GGAGCAGGGGAAGGGAAGGAATTTGCTTCTCAGATCATTTGGTCTTGGGATGGTG 4181  
DB 350 ----- 349  
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DB 350 -----GAGTCCCA 357

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DB 418 GAAGTACGGGTATGATGGCAGGACCACTTGAATTTCTGCCCTGCACACTGGATTGGAG 477  
QY 4362 AGCAGCAGAACCCAGGGCTGCGCCCAACCAAGCTGGAGTGGGAAAGGCAAGATTGGGC 4421  
DB 478 AGCAGCAGAACCCAGGGCTGCGCCCAACCAAGCTGGAGTGGGAAAGGCAAGATTGGGC 537  
QY 4422 CAGGAGCAGACAGGGCTTACCTCGAGAGGAGTGTCCCTGTCACAGTGTGACAGTTGCTGGA 4481  
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sequence.  
ACCESSION AQ296898  
VERSION AQ296898.1 GI:4014077  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 420)  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
Mahairas, G. C., Wallace, J. C., Smith, K., Swartzell, S., Holzman, T.,  
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M. D. and  
Hood, L.  
TITLE Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
MEDLINE 99380589  
PUBMED 10449764  
COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Sequence Tagged Connector  
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High quality sequence stop: 420.  
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Best Local Similarity 89.2%; Pred. No. 7.6e-35;  
Matches 357; Conservative 0; Mismatches 37; Indels 6; Gaps 4;  
QY 3075 AGGACCAAGCTGGGACGCTGGCTCACTTCTTAATCCAGCACTTTGGTGGCTGAGGC 3134



Db 1..ACGACCAAGCTGGGCA CGGTGGCTCACTTATGTAATCCACGACCTTTGGTGGCTGAGGC 60

Qy 3135 AGGTAGATCACTTGGGTCAGAGTTTGGAGCAAGCTTTGGCAACATCGTGAACCCCAT 3194

Db 61 ANGTAGATCACTTGGGTCAGAGTTTGGAGCAAGCTTTGGCAACATCGTGAACCCCAT 120

Qy 3195 GTCTACTAAAAATACAAAAATAGCTGGTGGTGGCGCACGCTATAGTCCAGGTTT 3254

Db 121 GTCTACTAAAAATACAAAAATAGCTGGTGGTGGCGCACGCTATAGTCCAGGTTT 180

Qy 3255 TCAGGAGCTTAGTGGAGAGTCCCTTGAACCCAGAGGTGCGAGTTGCGAGTGA 3314

Db 181 TCAGGAGCTTAGTGGAGAGTCCCTTGAACCCAGAGGTGCGAGTTGCGAGTGA 240

Qy 3315 GATTGTGCACTGCACTCCAGCTGGGTGATAGAGTGAAGTCTGTCTCAAA--AAAAA 3372

Db 241 GATTGTGCACTGCACTCCAGCTGGGTGATAGAGTGAAGTCTGTCTCAAGNCCATNAC 300

Qy 3373 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 3432

Db 301 TNCATACNCTCTTAAAAAATGAGGAAATATT-CTCAGGATTTGGTCTAA--TGCC 357

Qy 3433 TGACACCAACTCTGATTCACATACCATGCTAGACAC 3472

Db 358 CTGACACCAACTGCTGAG-TCAACTACCATGTTAACACAC 396

# RESULT 10 BC041839/c

LOCUS BC041839 3713 bp mRNA linear HTC 04-MAR-2003

DEFINITION Homo sapiens, similar to expressed sequence AW111961, clone

IMAGE:5268751, mRNA.

ACCESSION BC041839

VERSION BC041839.1 GI:27693117

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3713)

Strausberg, R.

Direct Submission

Submitted (23-DEC-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgapbs-x@mail.nih.gov](mailto:cgapbs-x@mail.nih.gov)

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki

Toehiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www.shgc.stanford.edu>

Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,

R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 74 Row: g Column: 3

This clone has the following problem: retained intron.

Location/Qualifiers

1..3713

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/clone\_lib="NIH\_MGC\_97"

/lab\_host="DH10B"

## FEATURES source

## ORIGIN

Query Match 5.6%; Score 281.6; DB 3; Length 3713;  
Best Local Similarity 65.6%; Pred. No. 2.2e-33;  
Matches 542; Conservative 0; Mismatches 23; Indels 50; Gaps 7;

/note="Vector: pBluescript"

Qy 2578 TGGCTGGGTGTAGTAGCTCATGCGCAAGGAGGAGCGCCAGGAGAGCAGATTCTCGAGCTCA 2637

Db 2275 TGGCTCATGCTGTAAATGCCAGCACTTTGGGAGGCGCGAGGCGAGAG-TACGAGGTCA 2217

Qy 2638 GGAGTTCAAGACCGACCTGGGCAACACAGCAAAAAACCCCTTCTCTACAAAAAATACAAAA 2697

Db 2216 AGAGATCAAGACCACTCTGGCCAACTGGTGAACCCCACTCTCTACTAAAAAATACAAAA 2157

Qy 2698 TTAGCTGGGTGTGGTGGCATGCACCTGTGATCTTAGCTACTCGGGAGGCTGAGGTGGAGG 2757

Db 2156 TTAGCTGGGTGTGGTGGCATGCACCTGTGATCTTAGCTACTCGGGAGGCTGAGGTGGAGG 2098

Qy 2758 GTATTGCTTGGAGCCAGCAAGTTCAGAGCTGAGGTGAGGAGGAGGAGGAGGAGGAGGAGG 2817

Db 2097 GAATCACTTGAACCTGGAGGTGGAGGTTCAGAGTGGAGGAGGAGGAGGAGGAGGAGG 2038

Qy 2818 AGCTAGGTGACAGAGCAAGACCCCTGTCTCCCTGACCCCTGAAAAAGAGAGAGGTTAA 2877

Db 2037 AGCTGGGCGACAGAGCAAGACTCCATCTCAAAACAACAACAACAACAACAACAACAACA 1978

Qy 2878 AGTTGACTTGTCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 2937

Db 1977 ATTAATATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1929

Qy 2938 CATTTCTGAGATGCTGAAGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2997

Db 1928 GATTCTCTCTTTCAGAAACCTGTTAGATGTTTATTTGGGTGCTGACACAATTAATACTACT 1869

Qy 2998 TTGGGACATGTTAAAGTTTGGAGATTCCAGTCAGGCTTCCAAAGTGGTGGAGGCCACATAGCA 3057

Db 1868 TTGTGACCAACAGCCCACTGTAACTCTAT----- 1840

Qy 3058 GTTCAGTGTGAAGATTTCAGGACCAAGCTGGGCAAGGCTGCTCACTCTCTGTATATCCAGC 3117

Db 1839 GGTGGTGTATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1780

Qy 3118 ACTTTT-GGTGGCTGAGCGAGGTAGATCATTTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 3176

Db 1779 ACTTTGGAGGCTGAGGCGAGGTGATCCTTTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTG 1720

Qy 3177 AACATGGTGAACCCCATGTCTACTATAAAATACAAAA--ATTAGCCTGGTGTGGTGGCGC 3234

Db 1719 AACATGGTGACACCCCTGTTCTTACTATAAAATACAAAAACATTAGCCAGGCGATGGTGGCAG 1660

Qy 3235 ACCGCTATAGTCCAGGCTTTTCAGGAGGCTTAGGTAGGAGAGTCCCTTTGAACCCAGGAGG 3294

Db 1659 GCACTTGTATATCCAGCTACTTTGGAGGCTGAGGCGAGAGAAATTTGCTTGAACCTGGGAGG 1600

Qy 3295 TGCAAGTTGCGAGTGAAGTGTGCGCACTGCA---CTCCAGCCTGGGTGATAGAGTG 3351

Db 1599 TGAGGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGT 1540

Qy 3352 AGACTCTGTCTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 3397

Db 1539 AGACACGGTTTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA 1494

## RESULT 11 AQ839831

LOCUS

DEFINITION

260L13-C47 CITB Homo sapiens genomic clone 260L13, genomic survey

sequence.

ACCESSION AQ839831

VERSION AQ839831.1 GI:6652463

KEYWORDS GSS.

SOURCE Homo sapiens (human)



ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 6146)  
AUTHORS Carten,J.D., Makalowska,I., Robbins,C.M., Scott,N., Sood,R.,  
Connors,T.D., Bonner,T.I., Smith,J.R., Faruque,M.U., Stephan,D.A.,  
Pinkett,H., Morgenbesser,S.D., Su,K., Graham,C., Gregory,S.G.,  
Williams,H., McDonald,L., Baxevasis,A.D., Klingler,K.W. and  
Landes,G.M.  
TITLE A 6-Mb high-resolution physical and transcription map encompassing  
the hereditary prostate cancer 1 (HPC1) region  
JOURNAL Genomics 64 (1), 1-14 (2000)  
MEDLINE 20175426  
PubMed 10708513  
COMMENT Contact: Carpten JD  
Cancer Genetics Branch  
National Human Genome Research Institute/National Institutes of  
Health  
Bldg. 36, Room 3D04, 36 Convent Drive, Bethesda, MD  
Tel: 301 435 5626  
Fax: 301 435 5465  
Email: jdc@nhgri.nih.gov  
Class: shotgun.  
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VERSION BM551225.1 GI:18788091  
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ORGANISM Homo sapiens  
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REFERENCE 1 (bases 1 to 793)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@rs@mail.nih.gov  
Tissue Procurement: ARCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
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BQ712091.1 GI:21850990
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1 (bases 1 to 972)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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VERSION
BE272926.1 GI:9147279
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 570)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
FEATURES
source

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## RESULT 3

US-08-834-497A-1  
; Sequence 1, Application US/08834497A  
; Patent No. 6140305  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Winston J.  
; APPLICANT: Drayna, Dennis T.  
; APPLICANT: Feder, John N.  
; APPLICANT: Gnirke, Andreas  
; APPLICANT: Ruddy, David  
; APPLICANT: Tsuchihashi, Zenta  
; APPLICANT: Wolff, Roger K.  
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/834,497A  
; FILING DATE: 04-APR-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/652,265  
; FILING DATE: 23-MAY-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/632,673  
; FILING DATE: 16-APR-1996  
; CLASSIFICATION: 514  
; APPLICATION NUMBER: US 08/630,912  
; FILING DATE: 04-APR-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Poissant, Brian M.  
; REGISTRATION NUMBER: 28,462  
; REFERENCE/DOCKET NUMBER: 8907-0056-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 1:  
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US-08-834-497A-1

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; Patent No. 6140305  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Winston J.  
; APPLICANT: Drayna, Dennis T.  
; APPLICANT: Feder, John N.  
; APPLICANT: Gnikre, Andreas  
; APPLICANT: Ruddy, David  
; APPLICANT: Tsuchihashi, Zenta  
; APPLICANT: Wolff, Roger K.  
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: FastSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/834,497A  
; FILING DATE: 04-APR-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
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; FILING DATE: 04-APR-1996  
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; ATTORNEY/AGENT INFORMATION:  
; NAME: Poissant, Brian M.  
; REGISTRATION NUMBER: 28,462  
; REFERENCE/DOCKET NUMBER: 8907-0056-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
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Patent No. 6228594  
GENERAL INFORMATION:  
APPLICANT: Thomas, Winston J.  
APPLICANT: Drayna, Dennis T.  
APPLICANT: Feder, John N.  
APPLICANT: Gnirke, Andreas  
APPLICANT: Rudy, David  
APPLICANT: Tsuchinashi, Zenta  
APPLICANT: Wolff, Roger K.  
TITLE OF INVENTION: Hereditary Hemochromatosis Gene  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect version 8  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09503,444A  
FILING DATE: 14-Feb-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/652,265  
FILING DATE: 23-May-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/632,673  
FILING DATE: 16-Apr-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/630,912  
FILING DATE: 04-Apr-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Poissant, Brian M.  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 8907-0088-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10825 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
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; Sequence 3, Application US/09503444A  
; Patent No. 6228594  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Winston J.  
; APPLICANT: Drayna, Dennis T.  
; APPLICANT: Feder, John N.  
; APPLICANT: Gnirke, Andreas  
; APPLICANT: Ruddy, David  
; APPLICANT: Tsuchihashi, Zenta  
; APPLICANT: Wolff, Roger K.  
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Wordperfect Version 8  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/503,444A  
; FILING DATE: 14-Feb-2000  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/652,265  
; FILING DATE: 23-May-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/632,673  
; FILING DATE: 16-Apr-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/630,912  
; FILING DATE: 04-Apr-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Poissant, Brian M.  
; REGISTRATION NUMBER: 28,462  
; REFERENCE/DOCKET NUMBER: 8907-0088-999  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-9741  
; TELEX: 66141  
; INFORMATION FOR SEQ ID NO: 3:  
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RESULT 8

US-08-724-394A-21  
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; Patent No. 5872237  
; GENERAL INFORMATION:  
; APPLICANT: Feder, John N.  
; APPLICANT: Krommal, Gregory S.  
; APPLICANT: Lauer, Peter M.  
; APPLICANT: Ruddy, David A.  
; APPLICANT: Thomas, Winston  
; APPLICANT: Tsuchihashi, Zenta  
; APPLICANT: Wolfe, Roger K.  
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1  
; TITLE OF INVENTION: Sequences and Antibodies Thereto  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/724,394A  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitts, Renee A.  
; REGISTRATION NUMBER: 35,136  
; REFERENCE/DOCKET NUMBER: 017957-000100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 246240 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: cDNA  
; FEATURE:

; NAME/KEY: misc feature  
; LOCATION: 1..246240  
; OTHER INFORMATION: /note= "HLA-H. CONTIG"  
US-08-724-394A-21  
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Db	193384	GGCTGGAAAATTAAGTATATGTTTGAACGTTTGAACGTAAATCTCTTTTCGG	193443		QY	2221	AATAAACAAAGTAGTGTGGGAGTAGAGCCCAAGAAAGTAGGTAAATGGGCTCAGAAAGGA	2280
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/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/724,394A
/ FILING DATE: 01-OCT-1996
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitts, Renee A.
/ REGISTRATION NUMBER: 35,136
/ REFERENCE/DOCKET NUMBER: 017957-000100
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-576-0200
/ TELEFAX: 415-576-0300
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 246240 base pairs
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US-08-724-394A-22

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Db	193924	TATGATTCTTAAACATCACACTGCATTAGAGGTTGAATAAATAATTTTCATGTTGAGCAG	193983
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 ; Patent No. 6025130  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Thomas, Winston J.  
 ; APPLICANT: Drayna, Dennis T.  
 ; APPLICANT: Feder, John N.  
 ; APPLICANT: Gnirke, Andreas  
 ; APPLICANT: Ruddy, David  
 ; APPLICANT: Tsuchihashi, Zenta  
 ; APPLICANT: Wolff, Roger K.  
 ; TITLE OF INVENTION: Hereditary Hemochromatosis Gene  
 ; NUMBER OF SEQUENCES: 44  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
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 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/652,265  
 ; FILING DATE: 23-MAY-1996  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Smith, William M.  
 ; REGISTRATION NUMBER: 30,223  
 ; REFERENCE/DOCKET NUMBER: 17957-000500  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 576-0200  
 ; TELEFAX: (415) 576-0300  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
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; NAME/KEY: -
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; LOCATION: replace(3872, "g")
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US-08-652-265-5

Query Match      100.0%; Score 4998.4; DB 3; Length 10825;
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QY      601  CTACCACTGAATGTCAGATAGGGTCCCTCGCCCCCAGAACCTGCCCCCTCCCGCGCTGT 660
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QY      661  CCGGCTCTGGAGTGACTTTTGAACCGGCCACTCCCTTCCCGCAACTAGMATGCTTT 720
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## RESULT 11

US-08-652-265-7  
; Sequence 7, Application US/08652265  
; Patent No. 6025130  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Winston J.  
; APPLICANT: Drayna, Dennis T.  
; APPLICANT: Feder, John N.  
; APPLICANT: Gnirke, Andreas  
; APPLICANT: Ruddy, David  
; APPLICANT: Teuchihaishi, Zenta

APPLICANT: Wolff, Roger K.  
TITLE OF INVENTION: Hereditary Hemochromatosis Gene  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,265  
FILING DATE: 23-MAY-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 17957-000500  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
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TOPOLOGY: linear  
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OTHER INFORMATION: /label= 24d1  
US-08-652-265-7

Query Match 100.0%; Score 4998.4; DB 3; Length 10825;  
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## RESULT 12

US-08-834-497A-5  
; Sequence 5, Application US/08834497A  
; Patent No. 6140305

## GENERAL INFORMATION:

; APPLICANT: Thomas, Winston J.  
; APPLICANT: Drayna, Dennis T.  
; APPLICANT: Feder, John N.  
; APPLICANT: Gnirke, Andreas  
; APPLICANT: Ruddy, David  
; APPLICANT: Teuchihaishi, Zenta  
; APPLICANT: Wolff, Roger K.  
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2811

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: FASTSEQ for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/834,497A  
FILING DATE: 04-APR-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/652,265  
FILING DATE: 23-MAY-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/632,673  
FILING DATE: 16-APR-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,912  
FILING DATE: 04-APR-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Poissant, Brian M.  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 8907-0056-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
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TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
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US-08-834-497A-5

Query Match 100.0%; Score 4998.4; DB 3; Length 10825;  
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Query Match 100.0%; Score 4998.4; DB 3; Length 10825;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 4999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
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DB	601	CTACCACTGAACTGACAGTAGGGTCCCTCGCCCCAGGACCTGCCCCCTCCCGGCTGT	660
QY	661	CCGGCTCTGCGGAGTGACTTTTGGAAACCGCCACTCCCTTCCCCCAACTAGAAATGCTTT	720
DB	661	CCGGCTCTGCGGAGTGACTTTTGGAAACCGCCACTCCCTTCCCCCAACTAGAAATGCTTT	720
QY	721	TAAATAAATCTCGTAGTCTCTCACTTGTAGTGAGCTTAAGCTGGGGCTCCTTGAACCTGG	780
DB	721	TAAATAAATCTCGTAGTCTCTCACTTGTAGTGAGCTTAAGCTGGGGCTCCTTGAACCTGG	780
QY	781	AATCGGGTTTATTTTCCAAATGTACGTGTGCTGCTTTTCCCGAGTCATCTCCAAACAGG	840
DB	781	AATCGGGTTTATTTTCCAAATGTACGTGTGCTTTCCTCCCGAGTCATCTCCAAACAGG	840
QY	841	AAGTTCTTCCCTGAGTGCTTGGCGAAGGCTGAGCAAAACCCACAGCAGGATCCGACCG	900
DB	841	AAGTTCTTCCCTGAGTGCTTGGCGAAGGCTGAGCAAAACCCACAGCAGGATCCGACCG	900
QY	901	GGTTTCCACTCAGAACGAATGCGTTGGCGGTGGGGCGCGAAAGAGTGGGCTGGGGA	960
DB	901	GGTTTCCACTCAGAACGAATGCGTTGGCGGTGGGGCGCGAAAGAGTGGGCTGGGGA	960
QY	961	TCTGAATTTCTACCAATTCACCCACTTTTGGTGAGACCTGGGGTGGAGGTCTTAGGGT	1020
DB	961	TCTGAATTTCTACCAATTCACCCACTTTTGGTGAGACCTGGGGTGGAGGTCTTAGGGT	1020
QY	1021	GGGAGGCTCTCTGAGAGAGGCTACCTCGGGCCCTTTCCCACTCTTTGGCAATTTCTTTT	1080

DB	1021	GGGAGGCTCTCTGAGAGAGGCTACCTCGGGCCCTTTCCCACTCTTTGGCAATTTCTTTT	1080
QY	1081	GCCTGGAAAAATTAAGTATATGTAGTTTGAAGGTTGAAGCTGAACAAATCTCTTTTCGG	1140
DB	1081	GCCTGGAAAAATTAAGTATATGTAGTTTGAAGGTTGAAGCTGAACAAATCTCTTTTCGG	1140
QY	1141	CTAGGCTTTATTTGATTTGCAATGTGCTGTAAATTAAGAGGCTCTCTCAAAAGTACTGA	1200
DB	1141	CTAGGCTTTATTTGATTTGCAATGTGCTGTAAATTAAGAGGCTCTCTCAAAAGTACTGA	1200
QY	1201	TAATGAACAATGAAGCAATGCACTCATCTTCTAAGTTTACATTCATATCTGATCTTATTTGA	1260
DB	1201	TAATGAACAATGAAGCAATGCACTCATCTTCTAAGTTTACATTCATATCTGATCTTATTTGA	1260
QY	1261	TTTTTCACTAGGCATAGGGAGGTAGGAGCTAAATAACGTTTATTTTACTAGAGTTAACT	1320
DB	1261	TTTTTCACTAGGCATAGGGAGGTAGGAGCTAAATAACGTTTATTTTACTAGAGTTAACT	1320
QY	1321	GGAAATTCAGATTTATATACTCTTTTTCAGGTTACAAAGAAACATAAATAATCTGTTTCTG	1380
DB	1321	GGAAATTCAGATTTATATACTCTTTTTCAGGTTACAAAGAAACATAAATAATCTGTTTCTG	1380
QY	1381	ATGTTATTTTCAAGTACTACAGCTGCTTTTAACTCTTATAGTTTGAAGTATTTGCCCCGTAG	1440
DB	1381	ATGTTATTTTCAAGTACTACAGCTGCTTTTAACTCTTATAGTTTGAAGTATTTGCCCCGTAG	1440
QY	1441	TGTAGCACAGTGTCTGTGGGTTCACACCGCGGCTTCAGCACAGCAGCTTTGAGTTTGGTA	1500
DB	1441	TGTAGCACAGTGTCTGTGGGTTCACACCGCGGCTTCAGCACAGCAGCTTTGAGTTTGGTA	1500
QY	1501	CTACGTGTATCCACATTTTACACATGACAAAGATAGGAGCATGGCAGCGCTGCTCTCTCG	1560
DB	1501	CTACGTGTATCCACATTTTACACATGACAAAGATAGGAGCATGGCAGCGCTGCTCTCTCG	1560
QY	1561	CAAAATTTTCAATCGTACACTGGGCTTTGTTGGCAGAGCTCATGTCTCCATTCATAGC	1620
DB	1561	CAAAATTTTCAATCGTACACTGGGCTTTGTTGGCAGAGCTCATGTCTCCATTCATAGC	1620
QY	1621	TATGATTTCTTAAACATCACCTGCACTTAGAGGTTGAAATAAATAATTTCTAGTGAGCAG	1680
DB	1621	TATGATTTCTTAAACATCACCTGCACTTAGAGGTTGAAATAAATAATTTCTAGTGAGCAG	1680
QY	1681	AAATATTTCAATCTTTTACCAAGTAAATGAGTCCCAAGCAGCATGTGTGCACTGTTCAAGCCC	1740
DB	1681	AAATATTTCAATCTTTTACCAAGTAAATGAGTCCCAAGCAGCATGTGTGCACTGTTCAAGCCC	1740
QY	1741	CAAGGAGAGAGCAGGGAAACAAAGTCTTTTACCCTTTGATATTTTGCATTTCTAGTGGGAGA	1800
DB	1741	CAAGGAGAGAGCAGGGAAACAAAGTCTTTTACCCTTTGATATTTTGCATTTCTAGTGGGAGA	1800
QY	1801	GATGCAATTAAGCAATGAGCAGAAAGATATACACATCAGGAAATCATGGGTGTTGTA	1860
DB	1801	GATGCAATTAAGCAATGAGCAGAAAGATATACACATCAGGAAATCATGGGTGTTGTA	1860
QY	1861	GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGGCTGACACTTTGAGCAGAGACATGAAGA	1920
DB	1861	GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGGCTGACACTTTGAGCAGAGACATGAAGA	1920
QY	1921	AATAAGAAATGATTTGACTGGGAGCAGTATTTTCCAGGCAAACTGAGTGGGCTGSCAAG	1980
DB	1921	AATAAGAAATGATTTGACTGGGAGCAGTATTTTCCAGGCAAACTGAGTGGGCTGSCAAG	1980
QY	1981	TTGGATTTAAAGCCGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGGG	2040
DB	1981	TTGGATTTAAAGCCGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGGG	2040
QY	2041	CGGCGTGGGGTGGGAAGGGGAGCTACCATCTGCACTAGGATGCTTAGCAGTATCTCT	2100
DB	2041	CGGCGTGGGGTGGGAAGGGGAGCTACCATCTGCACTAGGATGCTTAGCAGTATCTCT	2100
QY	2101	CTCCCTACTCTACTAGGTCTAGGAGCAGCTCCCGCAGTCTTGAACAACCAAAATGCTCT	2160
DB	2101	CTCCCTACTCTACTAGGTCTAGGAGCAGCTCCCGCAGTCTTGAACAACCAAAATGCTCT	2160











||||| 61 AATATCTAAAGTTTCAATCAGAACATTTGGAAAGCTACTTTTCCCAATCAACAAACCCCT 120  
QY ||||| 121 TCAGGATTTAAACCAAGGGGACACCTGGATCACCTAGTGTTCACAAAGCAGGTACCTT 180  
Db ||||| 121 TCAGGATTTAAACCAAGGGGACACCTGGATCACCTAGTGTTCACAAAGCAGGTACCTT 180  
QY ||||| 181 CTGCTGTAGGAGAGAGAGAACTAAAGTTCTGAAAGACCTGTGTCTTTTCAACAGGAAGTT 240  
Db ||||| 181 CTGCTGTAGGAGAGAGAGAACTAAAGTTCTGAAAGACCTGTGTCTTTTCAACAGGAAGTT 240  
QY ||||| 241 TTACTGGGCATCTCTGAGCCTAGGCAATAGCTGTAGGTGACTCTCGAGCCATCCCG 300  
Db ||||| 241 TTACTGGGCATCTCTGAGCCTAGGCAATAGCTGTAGGTGACTCTCGAGCCATCCCG 300  
QY ||||| 301 TTTCCCGCCCCCAAAAGAGCGGAGATTTAAACGGGACGTGCGGCCAGAGCTGGGAA 360  
Db ||||| 301 TTTCCCGCCCCCAAAAGAGCGGAGATTTAAACGGGACGTGCGGCCAGAGCTGGGAA 360  
QY ||||| 361 ATGGGCGCGAGCCAGGCGCGCTTCTCTCTGTATGCTTTTGCAGACCGCGTCTGT 420  
Db ||||| 361 ATGGGCGCGAGCCAGGCGCGCTTCTCTCTGTATGCTTTTGCAGACCGCGTCTGT 420  
QY ||||| 421 CAGGGCGCTTGCTCGGTGAGTCCGAGGCTGCGGGCGAATAGGGGCGCGCGGGGTG 480  
Db ||||| 421 CAGGGCGCTTGCTCGGTGAGTCCGAGGCTGCGGGCGAATAGGGGCGCGCGGGGTG 480  
QY ||||| 481 GAAAAATCGAAACTAGCTTTTCTTTGGCTTTGGGAGTTTGCTAACTTTGGAGACCTGC 540  
Db ||||| 481 GAAAAATCGAAACTAGCTTTTCTTTGGCTTTGGGAGTTTGCTAACTTTGGAGACCTGC 540  
QY ||||| 541 TCAAACCTATCCGGAAGCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGGAGTGC 600  
Db ||||| 541 TCAAACCTATCCGGAAGCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGGAGTGC 600  
QY ||||| 601 CTACACCTGAACTGAGAGTGGGTCTCCCTGCGCCAGAGACCTGCGCCCTCCCGGCTGT 660  
Db ||||| 601 CTACACCTGAACTGAGAGTGGGTCTCCCTGCGCCAGAGACCTGCGCCCTCCCGGCTGT 660  
QY ||||| 661 CCGGCTCTGGGAGTGACTTTTGAACCGCCACTCCCTTCCGCCAACTAGAATGCTTT 720  
Db ||||| 661 CCGGCTCTGGGAGTGACTTTTGAACCGCCACTCCCTTCCGCCAACTAGAATGCTTT 720  
QY ||||| 721 TAAATAATCTGTAAGTTCTCTCCTACTGAGCTGAGCTTAAGCCTGGGGCTCTTGAACCTGG 780  
Db ||||| 721 TAAATAATCTGTAAGTTCTCTCCTACTGAGCTGAGCTTAAGCCTGGGGCTCTTGAACCTGG 780  
QY ||||| 781 AACTCGGGTTTATTTTCCAATGTCAGTGTGCAAGTTTTTCCCACTCATCTCCAACAGG 840  
Db ||||| 781 AACTCGGGTTTATTTTCCAATGTCAGTGTGCAAGTTTTTCCCACTCATCTCCAACAGG 840  
QY ||||| 841 AAGTTCTTCCCTGAGTGTTCGAGAGAGGCTGAGCAAAACCAACAGAGGATCCGACGG 900  
Db ||||| 841 AAGTTCTTCCCTGAGTGTTCGAGAGAGGCTGAGCAAAACCAACAGAGGATCCGACGG 900  
QY ||||| 901 GGTTCACACTCAGAAAGAAAGCTGTGGCGGTGGGGCGGAAAGAGTGGGTGGGGA 960  
Db ||||| 901 GGTTCACACTCAGAAAGAAAGCTGTGGCGGTGGGGCGGAAAGAGTGGGTGGGGA 960  
QY ||||| 961 TCTGAATTTCTTCAACATTTCCCACTTTTGGTGAGACTGGGGTGGAGGTCTCTAGGT 1020  
Db ||||| 961 TCTGAATTTCTTCAACATTTCCACCTTTTGGTGAGACTGGGGTGGAGGTCTCTAGGT 1020  
QY ||||| 1021 GGGAGGCTCTGAGAGAGCCTTACCTCGGGCTTTTCCCACTCTTTGGCAATGTTCTTTT 1080  
Db ||||| 1021 GGGAGGCTCTGAGAGAGCCTTACCTCGGGCTTTTCCCACTCTTTGGCAATGTTCTTTT 1080  
QY ||||| 1081 GCCTGGAAATTAAGTATATGTAGTTTGAACGTTTGAACGAAATTTCTCTTTTGG 1140  
Db ||||| 1081 GCCTGGAAATTAAGTATATGTAGTTTGAACGTTTGAACGAAATTTCTCTTTTGG 1140  
QY ||||| 1141 CTAGGCTTTATTTGATTTGCAATGTGCTGTAAATTAAGAGGCTCTCTACAAAGTACTGA 1200

Db ||||| 1141 CTAGGCTTTATTTGATTTGCAATGTGCTGTAAATTAAGAGGCTCTCTACAAAGTACTGA 1200  
QY ||||| 1201 TAAATGAACATTAAGCAATGCACTCACTTTCTAAGTTTACATTCATATCTGATCTTATTTGA 1260  
Db ||||| 1201 TAAATGAACATTAAGCAATGCACTCACTTTCTAAGTTTACATTCATATCTGATCTTATTTGA 1260  
QY ||||| 1261 TTTTTCATCTAGGACATAGGAGGTAGGAGCTAATAACGTTTATTTTACTAGAGTTAACT 1320  
Db ||||| 1261 TTTTTCATCTAGGACATAGGAGGTAGGAGCTAATAACGTTTATTTTACTAGAGTTAACT 1320  
QY ||||| 1321 GGAATTCAGATTAATAAATCTTTTTCAGGTTACAAAGAAACATAAATAATCTGGTTTTCTG 1380  
Db ||||| 1321 GGAATTCAGATTAATAAATCTTTTTCAGGTTACAAAGAAACATAAATAATCTGGTTTTCTG 1380  
QY ||||| 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTGTAGTGAAGTATTTTGGCCTGTAG 1440  
Db ||||| 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTGTAGTGAAGTATTTTGGCCTGTAG 1440  
QY ||||| 1441 TGTAGCACAGTGTCTGTGGGTCAACGCGGCTTCAGCAGGACACTTTGAGTTTGGTA 1500  
Db ||||| 1441 TGTAGCACAGTGTCTGTGGGTCAACGCGGCTTCAGCAGGACACTTTGAGTTTGGTA 1500  
QY ||||| 1501 CTAGCTGTATCCACATTTTACACATGACAAAGATGAGGCATGCGACGCTTCTCTGG 1560  
Db ||||| 1501 CTAGCTGTATCCACATTTTACACATGACAAAGATGAGGCATGCGACGCTTCTCTGG 1560  
QY ||||| 1561 CAAATTTATTTCAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620  
Db ||||| 1561 CAAATTTATTTCAATGGTACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620  
QY ||||| 1621 TATGATTTCTTAAACATCAGCTGCACTTATGAGGTTGAATAATAAATTTTCAATGTGAGCAG 1680  
Db ||||| 1621 TATGATTTCTTAAACATCAGCTGCACTTATGAGGTTGAATAATAAATTTTCAATGTGAGCAG 1680  
QY ||||| 1681 AAATATTTCAATTTTACAAAGTGTAAATGAGTCCAGGCACTGTGTGCACTGTTCGAAGCCC 1740  
Db ||||| 1681 AAATATTTCAATTTTACAAAGTGTAAATGAGTCCAGGCACTGTGTGCACTGTTCGAAGCCC 1740  
QY ||||| 1741 CAAGGAGAGAGCAGGGGAAACAAGTCTTTTACCTTTGATATTTTGGCATCTTAGTGGGAGA 1800  
Db ||||| 1741 CAAGGAGAGAGCAGGGGAAACAAGTCTTTTACCTTTGATATTTTGGCATCTTAGTGGGAGA 1800  
QY ||||| 1801 GATGACAAATAGCAAAATGAGCAGAAAGATATACAAATCATGAGAAATCATGGTGTGTGA 1860  
Db ||||| 1801 GATGACAAATAGCAAAATGAGCAGAAAGATATACAAATCATGAGAAATCATGGTGTGTGA 1860  
QY ||||| 1861 GAAGCAGAGAAAGTCAGGGCAAGTCACTCTGGGGCTGACACTTGGAGCAGAGACATGAAGGA 1920  
Db ||||| 1861 GAAGCAGAGAAAGTCAGGGCAAGTCACTCTGGGGCTGACACTTGGAGCAGAGACATGAAGGA 1920  
QY ||||| 1921 AATAAGAAATGATATTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAAG 1980  
Db ||||| 1921 AATAAGAAATGATATTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAAG 1980  
QY ||||| 1981 TTGGATTTAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040  
Db ||||| 1981 TTGGATTTAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040  
QY ||||| 2041 CCGGCTGGGGGTGGGAAGGGGACTTACCATCTGCATGTAGGATGTCTTAGCAGTATCTCTGT 2100  
Db ||||| 2041 CCGGCTGGGGGTGGGAAGGGGACTTACCATCTGCATGTAGGATGTCTTAGCAGTATCTCTGT 2100  
QY ||||| 2101 CCTCCCTACTCATAGTGTCTAGGAGCACTCCCGCAGTCTTGACAAACCAAAATGTCTCT 2160  
Db ||||| 2101 CCTCCCTACTCATAGTGTCTAGGAGCACTCCCGCAGTCTTGACAAACCAAAATGTCTCT 2160  
QY ||||| 2161 AAATTTTCCCACTGTCACTTAGTAGCAAACTCTCTGGTTAAGAGCTCGGGTGAAGAA 2220  
Db ||||| 2161 AAATTTTCCCACTGTCACTTAGTAGCAAACTCTCTGGTTAAGAGCTCGGGTGAAGAA 2220  
QY ||||| 2221 AATAAACAAAGTGTCTGGGAGTAGAGGCGCAAGAAAGTGTGTAAATGGGCTCAGAAAGAGA 2280  
Db ||||| 2221 AATAAACAAAGTGTCTGGGAGTAGAGGCGCAAGAAAGTGTGTAAATGGGCTCAGAAAGAGA 2280



Qy	2281	GCCACAAACAGGTTGTGCAGGCCCTGTAGGCTGTGGTGTGAATTTCTAGCCAAAGAGTA	2340
Db	2281	GCCACAAACAGGTTGTGCAGGCCCTGTAGGCTGTGGTGTGAATTTCTAGCCAAAGAGTA	2340
Qy	2341	ACAGTGATCTGTCA CAGGCTTTTAAAAAGATTGCTCTGGCTGCTATGTGGAAAGCAGAAATG	2400
Db	2341	ACAGTGATCTGTCA CAGGCTTTTAAAAAGATTGCTCTGGCTGCTATGTGGAAAGCAGAAATG	2400
Qy	2401	AAGGGAGCAACAGTAAAGCAGGAGGCCACGAGGAAGCTGTGTACACAGTCAGGCAAG	2460
Db	2401	AAGGGAGCAACAGTAAAGCAGGAGGCCACGAGGAAGCTGTGTACACAGTCAGGCAAG	2460
Qy	2461	AGGTAGTGGAGTGGGCTGGGAAACAGAAAGGGAGTCACAAACATTTGTCTCTGAA	2520
Db	2461	AGGTAGTGGAGTGGGCTGGGAAACAGAAAGGGAGTCACAAACATTTGTCTCTGAA	2520
Qy	2521	TATATTTCTGAAGGAAGTTGCTGAAGGATTTCTATGTGTGTGAGAGAAAGAGAAGAAATGG	2580
Db	2521	TATATTTCTGAAGGAAGTTGCTGAAGGATTTCTATGTGTGTGAGAGAAAGAGAAGAAATGG	2580
Qy	2581	CTGGGTGTAGTAGTCAATGCAAGGAGGAGGCCAAGGAGACAGATTCCTGAGCTCAGGA	2640
Db	2581	CTGGGTGTAGTAGTCAATGCAAGGAGGAGGCCAAGGAGACAGATTCCTGAGCTCAGGA	2640
Qy	2641	GTTCAAGACAGCCTGGGCAACACAGCAAAACCCCTCTCTACAAATAATACAAAATTA	2700
Db	2641	GTTCAAGACAGCCTGGGCAACACAGCAAAACCCCTCTCTACAAATAATACAAAATTA	2700
Qy	2701	GCTGGGTGTGGTGGCATGCCTGTGATCTCTAGTACTTCGGGAGGCTGAGGTGGAGGTA	2760
Db	2701	GCTGGGTGTGGTGGCATGCCTGTGATCTCTAGTACTTCGGGAGGCTGAGGTGGAGGTA	2760
Qy	2761	TTGCTTGAGCCACAGGAAGTTGAGGCTGCAGTAGCCACATGCTGCCACTGTACTTCAGC	2820
Db	2761	TTGCTTGAGCCACAGGAAGTTGAGGCTGCAGTAGCCACATGCTGCCACTGTACTTCAGC	2820
Qy	2821	CTAGGTGACAGACAGACACCTGTGTCTCCCTGACCCCTGAAAAGAGAGAGCTTAAAGT	2880
Db	2821	CTAGGTGACAGACAGACACCTGTGTCTCCCTGACCCCTGAAAAGAGAGAGCTTAAAGT	2880
Qy	2881	TGACTTTGTTCTTTTATTTTAAATTTATTTGGCCTGAGCAGTGGGGTAAATTTGGCAATGCCAT	2940
Db	2881	TGACTTTGTTCTTTTATTTTAAATTTATTTGGCCTGAGCAGTGGGGTAAATTTGGCAATGCCAT	2940
Qy	2941	TTCTGAGATGGTGAAGGCAGAGAAAGAGCAGATTTGGGGTAAATCAAGGATCTGCATTTTG	3000
Db	2941	TTCTGAGATGGTGAAGGCAGAGAAAGAGCAGATTTGGGGTAAATCAAGGATCTGCATTTTG	3000
Qy	3001	GGACATGTTAAATTTTGAGATTTCCAGTTCAGCTCAGGCTTCCAAAGTGGTCAGGCCACATAGGCAGTT	3060
Db	3001	GGACATGTTAAATTTTGAGATTTCCAGTTCAGCTCAGGCTTCCAAAGTGGTCAGGCCACATAGGCAGTT	3060
Qy	3061	CAGTGTAAAGAAATTCAGGACCAAGGCTGGGCA CGGTGGCTCACTTCTGTAAATCCAGCACT	3120
Db	3061	CAGTGTAAAGAAATTCAGGACCAAGGCTGGGCA CGGTGGCTCACTTCTGTAAATCCAGCACT	3120
Qy	3121	TTGGTGGCTGAGGAGGTAGATCAATTTGAGGTCAGAGGTTTGAGACAAGCTTGGGCAACA	3180
Db	3121	TTGGTGGCTGAGGAGGTAGATCAATTTGAGGTCAGAGGTTTGAGACAAGCTTGGGCAACA	3180
Qy	3181	TGGTGAACCCCATGTCTACTAAAAATACAAAAATTTAGCCTGTGTGTGGGCACGCT	3240
Db	3181	TGGTGAACCCCATGTCTACTAAAAATACAAAAATTTAGCCTGTGTGTGGGCACGCT	3240
Qy	3241	ATAGTCCCAGGTTTTTCAGGAGGCTTAGTTAGGAGAATTCCTTGAACCCAGGAGGTGCAG	3300
Db	3241	ATAGTCCCAGGTTTTTCAGGAGGCTTAGTTAGGAGAATTCCTTGAACCCAGGAGGTGCAG	3300
Qy	3301	TTGAGTGAGCTGAGATTGTGCCACTGCACCTCCAGCTGGGTGATAGATGAGACTCTGT	3360
Db	3301	TTGAGTGAGCTGAGATTGTGCCACTGCACCTCCAGCTGGGTGATAGATGAGACTCTGT	3360







Db 61 AATATCTAAAGTTTCAATCAGAACATTTGGGAAGCTACTTTCCCAATCAACAACCCCT 120  
Qy |||||  
Db 121 TCAGGATTTTAAACAACAGGGGACACTGGATCACCTAGTGTTCACAAGCAGGTACCTT 180  
Qy |||||  
Db 121 TCAGGATTTTAAACAACAGGGGACACTGGATCACCTAGTGTTCACAAGCAGGTACCTT 180  
Qy |||||  
Db 181 CTGCTGTAGGAGAGAGAACTAAAGTTCTCTGAAAGACCTGTTGCTTTTCCACAGGAAGTT 240  
Qy |||||  
Db 181 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTTGCTTTTCCACAGGAAGTT 240  
Qy |||||  
Db 241 TTACTGGGATCTCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGAGGCATCCCCG 300  
Qy |||||  
Db 241 TTACTGGGATCTCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGAGGCATCCCCG 300  
Qy |||||  
Db 301 TTTTCCCGCCCCCAAAAGAGCGAGATTTAAACGGGACGCTGCGCCAGAGCTGGGAA 360  
Qy |||||  
Db 301 TTTTCCCGCCCCCAAAAGAGCGAGATTTAAACGGGACGCTGCGCCAGAGCTGGGAA 360  
Qy |||||  
Db 361 ATGGGCCCGCGAGCCAGGCGCGCTTCTCTCTGATGCTTTTTCAGACCGCGTCTTG 420  
Qy |||||  
Db 361 ATGGGCCCGCGAGCCAGGCGCGCTTCTCTCTGATGCTTTTTCAGACCGCGTCTTG 420  
Qy |||||  
Db 421 CAGGGCGCTTGTGCTGAGTCCGAGGGCTGCGGCGCAACTAGGGGCGCGCGGGGTG 480  
Qy |||||  
Db 421 CAGGGCGCTTGTGCTGAGTCCGAGGGCTGCGGCGCAACTAGGGGCGCGCGGGGTG 480  
Qy |||||  
Db 481 GAAATTCGAACTAGCTTTTCTTTGCGCTTTGGGAGTTTGTAACTTTTGGAGGACCTGC 540  
Qy |||||  
Db 481 GAAATTCGAACTAGCTTTTCTTTGCGCTTTGGGAGTTTGTAACTTTTGGAGGACCTGC 540  
Qy |||||  
Db 541 TCACCCCTATCCGCAAGCCCTCTCCCTACTTTTCTGCGTCCAGACCCCGTGAGGGAGTGC 600  
Qy |||||  
Db 541 TCACCCCTATCCGCAAGCCCTCTCCCTACTTTTCTGCGTCCAGACCCCGTGAGGGAGTGC 600  
Qy |||||  
Db 601 CTACCACTGAACTGCAGATAGGGGTCCCTGCGCCCAAGGACCTGCCCCCTCCCGGCTGT 660  
Qy |||||  
Db 601 CTACCACTGAACTGCAGATAGGGGTCCCTGCGCCCAAGGACCTGCCCCCTCCCGGCTGT 660  
Qy |||||  
Db 661 CCGGCTCTCGGGAGTACTTTTGGNACCGCCCACTCCCTTCCCTCCCACTAGAACTGCTTT 720  
Qy |||||  
Db 661 CCGGCTCTCGGGAGTACTTTTGGNACCGCCCACTCCCTTCCCTCCCACTAGAACTGCTTT 720  
Qy |||||  
Db 721 TAAATAAATCTGCTAGTCTCTCACTGAGCTGAGCTTAAGCTGGGCTCTCTTGAACCTGG 780  
Qy |||||  
Db 721 TAAATAAATCTGCTAGTCTCTCACTGAGCTGAGCTTAAGCTGGGCTCTCTTGAACCTGG 780  
Qy |||||  
Db 781 AACTCGGGTTATTTCCAAATGTCAGCTGTGCAAGTCTTTTCCCAAGTCTCTCCAAACAGG 840  
Qy |||||  
Db 781 AACTCGGGTTATTTCCAAATGTCAGCTGTGCAAGTCTTTTCCCAAGTCTCTCCAAACAGG 840  
Qy |||||  
Db 841 AAGTTCTTCCCTGAGTGTCTCGGAGAGGCTGAGCAAAACCCACAGCAGGATCCGACGG 900  
Qy |||||  
Db 841 AAGTTCTTCCCTGAGTGTCTCGGAGAGGCTGAGCAAAACCCACAGCAGGATCCGACGG 900  
Qy |||||  
Db 901 GGTTTCCCACTCAGAACCAATGCTTTGGCGGTGGGGCGGCAAGAGTGGGCTTGGGA 960  
Qy |||||  
Db 901 GGTTTCCCACTCAGAACCAATGCTTTGGCGGTGGGGCGGCAAGAGTGGGCTTGGGA 960  
Qy |||||  
Db 961 TCTGAATTTCTCACCATTCCACCACTTTTGTGTGAGACCTGGGGTGGAGGTCTCTAGGGT 1020  
Qy |||||  
Db 961 TCTGAATTTCTCACCATTCCACCACTTTTGTGTGAGACCTGGGGTGGAGGTCTCTAGGGT 1020  
Qy |||||  
Db 1021 GGGAGGCTCTGAGAGAGGCTTACCTCGGGCTTTTCCCACTCTTGGGCAATTTGCTTTT 1080  
Qy |||||  
Db 1021 GGGAGGCTCTGAGAGAGGCTTACCTCGGGCTTTTCCCACTCTTGGGCAATTTGCTTTT 1080  
Qy |||||  
Db 1081 GCTGGAATTTAAGTATATGTTAGTTTGAAGCTTTGAAGTGAACAATTTCTCTTTTGG 1140  
Qy |||||  
Db 1081 GCTGGAATTTAAGTATATGTTAGTTTGAAGCTTTGAAGTGAACAATTTCTCTTTTGG 1140  
Qy |||||  
Db 1141 CTAGGCTTTATTTGATTTGCAATGTGCTGTGTAATTAAGAGGGCTCTCTACAAAGTACTGA 1200  
Qy |||||

Db 1141 CTAGGCTTTATTTGATTTGCAATGTGCTGTGTAATTAAGAGGGCTCTCTACAAAGTACTGA 1200  
Qy |||||  
Db 1201 TAAATGAACATGTAAAGCAATGCACTCACTTCTAAGTTTACATTTCAATCTCATTTTGA 1260  
Qy |||||  
Db 1201 TAAATGAACATGTAAAGCAATGCACTCACTTCTAAGTTTACATTTCAATCTCATTTTGA 1260  
Qy |||||  
Db 1261 TTTTTCACCTAGGCATAGGGAGGTAGGAGCTAAATAACGTTTATTTTACTAGAGTTAACT 1320  
Qy |||||  
Db 1261 TTTTTCACCTAGGCATAGGGAGGTAGGAGCTAAATAACGTTTATTTTACTAGAGTTAACT 1320  
Qy |||||  
Db 1321 GGAATTCAGATTTATATACTCTTTTTCAGGTTTCAAGAAACATAATAATCTGGTTCTG 1380  
Qy |||||  
Db 1321 GGAATTCAGATTTATATACTCTTTTTCAGGTTTCAAGAAACATAATAATCTGGTTCTG 1380  
Qy |||||  
Db 1381 ATGTTTATTTTCAAGTACTACAGCTGCTTCTAACTTTAGTTTGAAGTATTTTCCCTGTAG 1440  
Qy |||||  
Db 1381 ATGTTTATTTTCAAGTACTACAGCTGCTTCTAACTTTAGTTTGAAGTATTTTCCCTGTAG 1440  
Qy |||||  
Db 1441 TGTAGCAGAGTGTCTGTGGGTCAACGCGGCTTCAGCACAGCACCTTTTGTAGTTTGGTA 1500  
Qy |||||  
Db 1441 TGTAGCAGAGTGTCTGTGGGTCAACGCGGCTTCAGCACAGCACCTTTTGTAGTTTGGTA 1500  
Qy |||||  
Db 1501 CTACGTGTATCCACATTTTACATGACAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1560  
Qy |||||  
Db 1501 CTACGTGTATCCACATTTTACATGACAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1560  
Qy |||||  
Db 1561 CAAATTTTATTTCAAGTACTACAGCTGCTTCTAACTTTAGTTTGAAGTATTTTCCCTGTAG 1620  
Qy |||||  
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Qy |||||  
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QY	2521	TATATTCT	GAAAGGAAGTTGCTGTAAGGAATCTATGTTGTCAGAGAAGAGAAAGMATTTG	2580		
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QY	2761	TTGCTTG	AGCCACAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTCAGC	2820		
DB	2761	TTGCTTG	AGCCACAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTCAGC	2820		
QY	2821	CTAGGTG	CACAGACAAGACCTGTCTCCCTGACCCCTGAAAAGAGAGAAGTTAAAGT	2880		
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QY		3661	CCAGACACAGCTGATGGTATGAGTTGATGCAGGTGTGTGGAGCTCAA CATCTCGTCTCCC	3720
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Dd		3721	CTCCTACTACATGTTTAAAGGCTGTGTCTGTCTCTCCAGGTTCACTCTCTCGCACTA	3780
QY		3781	CCTCTTCATGGGTGCCCTCAGACAGAGNACCTTGGTCTTTTCTGTGTTTGAAGCTTTGGGCTA	3840
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NUC

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Searched: 6067389 seqs, 312528755 residues

Total number of hits satisfying chosen parameters: 12134778

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	4998.4	100.0	10825	15	US-10-138-888-79
6	4988	99.8	235033	15	US-10-301-844-1
7	4965.6	99.3	21608	21	US-10-741-600-17631

c	8	4958.8	99.2	237326	15	US-10-301-844-2	Sequence 2, Appli
	9	4957.2	99.1	12146	10	US-09-981-606-27	Sequence 27, Appl
	10	4607.8	92.2	15982	13	US-10-016-634A-25	Sequence 25, Appl
	11	2556.4	51.1	8622	15	US-10-311-455-2115	Sequence 2115, Ap
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	18	321	6.4	1440	15	US-10-138-888-9	Sequence 9, Appli
	19	321	6.4	1440	15	US-10-138-888-10	Sequence 10, Appl
	20	321	6.4	2506	10	US-09-981-606-1	Sequence 1, Appli
	21	321	6.4	2739	21	US-10-956-250-1	Sequence 11, Appl
	22	319.4	6.4	1440	15	US-10-138-888-11	Sequence 12, Appl
	23	319.4	6.4	1440	15	US-10-138-888-12	Sequence 77, Appl
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	25	316.6	6.3	2285	21	US-10-741-600-271	Sequence 271, App
	26	316.6	6.3	2674	21	US-10-741-600-267	Sequence 267, App
	27	316.6	6.3	2716	21	US-10-741-600-265	Sequence 265, App
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	31	307.8	6.1	379652	21	US-10-481-613-71	Sequence 7069, Ap
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c	33	302.6	6.1	39428	20	US-10-719-993-7069	Sequence 281, App
c	34	302.4	6.0	167343	9	US-09-962-436-281	Sequence 273, App
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	41	300	6.0	124990	20	US-10-684-422-156	Sequence 17708, A
	42	299.8	6.0	148935	21	US-10-741-600-17708	Sequence 17777, A
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#### ALIGNMENTS

#### RESULT 1

US-10-138-888-1  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Winston J.  
; Drayna, Dennis T.  
; Feder, John N.  
; Gnirke, Andreas  
; Ruddy, David  
; Tsuchihashi, Zenta  
; Wolff, Roger K.  
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene  
; NUMBER OF SEQUENCES: 79  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/138,888  
; FILING DATE: 02-May-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/834,497











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RESULT 2  
US-10-138-888-3  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Winston J.  
; Drayna, Dennis T.  
; Feder, John N.  
; Gnirke, Andreas  
; Ruddy, David  
; Tsuchihashi, Zenta  
; Wolff, Roger K.  
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene  
; NUMBER OF SEQUENCES: 79  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/138,888  
; FILING DATE: 02-May-2002  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/834,497  
; FILING DATE: 04-APR-1997  
; APPLICATION NUMBER: US 08/652,265  
; FILING DATE: 23-MAY-1996  
; APPLICATION NUMBER: US 08/632,673  
; FILING DATE: 16-APR-1996  
; APPLICATION NUMBER: US 08/630,912  
; FILING DATE: 04-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brian M. Poissant  
; REGISTRATION NUMBER: 28,462  
; REFERENCE/DOCKET NUMBER: 8907-095-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; OTHER INFORMATION: /product= "Hereditary Hemochromatosis  
; (HH) protein containing the 24d1  
; mutation"  
; /note= "Hereditary Hemochromatosis (HH)  
; gene 24d1 allele"  
; FEATURE:  
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RESULT 3

US-10-138-888-5

GENERAL INFORMATION:

APPLICANT: Thomas, Winston J.  
Drayna, Dennis T.  
Feder, John N.  
Girke, Andreas  
Ruddy, David  
Tsuchihashi, Zenta  
Wolff, Roger K.  
TITLE OF INVENTION: Hereditary Hemochromatosis Gene  
NUMBER OF SEQUENCES: 79  
CORRESPONDENCE ADDRESS:  
ADDRESS: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/138,888  
FILING DATE: 02-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/834,497  
FILING DATE: 04-APR-1997  
APPLICATION NUMBER: US 08/652,265  
FILING DATE: 23-MAY-1996  
APPLICATION NUMBER: US 08/632,673  
FILING DATE: 16-APR-1996  
APPLICATION NUMBER: US 08/630,912  
FILING DATE: 04-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Brian M. Poissant  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 8907-095-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
OTHER INFORMATION: /product= "Hereditary Hemochromatosis (HH) protein containing the 24d2 mutation"  
/note= "Hereditary Hemochromatosis (HH) gene 24d2 allele"  
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US-10-138-888-5  
Query Match 100.0%; Score 4998.4; DB 15; Length 10825;  
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Qy 4981 GCTAATTGGAAGCTCAGGC 5000  
Db 4981 GCTAATTGGAAGCTGAGGC 5000

RESULT 4

US-10-138-888-7

GENERAL INFORMATION:

APPLICANT: Thomas, Winston J.  
Drayna, Dennis T.  
Feder, John N.  
Girke, Andreas  
Ruddy, David  
Tsuchihashi, Zenta  
Wolff, Roger K.  
TITLE OF INVENTION: Hereditary Hemochromatosis Gene  
NUMBER OF SEQUENCES: 79  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/138,888  
FILING DATE: 02-May-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/834,497  
FILING DATE: 04-APR-1997  
APPLICATION NUMBER: US 08/652,265  
FILING DATE: 23-MAY-1996  
APPLICATION NUMBER: US 08/632,673  
FILING DATE: 16-APR-1996  
APPLICATION NUMBER: US 08/630,912  
FILING DATE: 04-APR-1996

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REFERENCE/DOCKET NUMBER: 8907-095-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864

OTHER INFORMATION: /product= "Hereditary Hemochromatosis (HH) protein containing both the 24d1 and 24d2 mutations"  
/note= "Hereditary Hemochromatosis (HH) gene containing a combination of both 24d1 and 24d2 alleles"

FEATURE:

NAME/KEY: -  
LOCATION: 140..7319  
FEATURE:  
NAME/KEY: -  
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NAME/KEY: allele  
LOCATION: replace(5834, "a")  
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis (HH)"  
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SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-138-888-7  
Query Match 100.0%; Score 4998.4; DB 15; Length 10825;  
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Matches 4999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Qy 181 CTGCTGTAGGAGAGAGAGAACTAAAGTTCTGAAAGACCTGTGCTTTTACCAGGAAGTT 240  
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Qy 361 ATGGGCCCGGAGCCAGCCGCGCTTCTCTCTGATGCTTTTGACACCGCGTCTCTG 420  
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Db 781 AACTCGGGTTTATTTTCAATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 840  
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Db 841 AAGTTCTTCCCTGAGTGTGCTCGGAGAGGCTGAGCAAAACCCACAGCAGGATCCCAAG 900  
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Db 901 GGTTCACACTCAGAACGAATCGCTTGGCGGTGGGGCGCGAAGAGTGGCTTGGGGA 960  
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	1021	GGGAGGCTCCTGAGAGAGGCTACTCGGGCTTTCCCCACTCTGTGGCAATGTGTTCTTTT	1080
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	1141	CTAGGCTTTATTGATTTGCAATGCTGTGTAAATTAGAGGCGCTCTCTACAAAGTACTGA	1200
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	1321	GGAAATTCAGATTAATAACTCTTTTTCAGGTTTACAAGAACTAATAATCTGTGTTTCTG	1380
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	1441	TGTAGCACAGTGTCTGTGGGTACACCGCGGCTCAGCACAGCACTTTGAGTTTGGTA	1500
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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/138,888  
Filing DATE: 02-May-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/834,497  
Filing DATE: 04-APR-1997  
APPLICATION NUMBER: US 08/652,265  
Filing DATE: 23-MAY-1996  
APPLICATION NUMBER: US 08/632,673  
Filing DATE: 16-APR-1996  
APPLICATION NUMBER: US 08/630,912  
Filing DATE: 04-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Brian M. Poissant  
REGISTRATION NUMBER: 28,462  
REFERENCE/DOCKET NUMBER: 8907-095-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
OTHER INFORMATION: /product= "Hereditary Hemochromatosis  
(HH) protein containing the 24d7 mutation"  
/note= "Hereditary Hemochromatosis  
(HH) gene 24d7 allele"  
FEATURE:  
NAME/KEY: -  
LOCATION: 140..7319  
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LOCATION: 5507..6023  
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LOCATION: replace(3878, "t")  
OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis  
(HH)"  
/label= 24d7  
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Query Match 100.0%; Score 4998.4; DB 15; Length 10825;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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4441 CTGGAGAGGGGACTGCCCTTGCAAGCTGCAAGCTGTCAGAGCTTTGCTGGAGCTGGGGAGAGTGTGTTG 4500











|||||  
Db 9279 TCTAATTTGCCCTGAGCACCACCTCTCTGAGTTCAACTACCTAGCTAGACACACCTTTAAC 9338  
Qy 3481 ATTTTCTAGAATCCACCAGCTTTAGTGAGTCTGTCTAATCATGAGTATTTGGAATPAGAT 3540  
Db 9339 ATTTTCTAGAATCCACCAGCTTTAGTGAGTCTGTCTAATCATGAGTATTTGGAATPAGAT 9398  
Qy 3541 CTGGGGGCACTGAGGGGTGGCAGCCACGTTGTGGCAGAGAAAGACACACAGGAAAGAGC 3600  
Db 9399 CTGGGGGCACTGAGGGGTGGCAGCCACGTTGTGGCAGAGAAAGACACACAGGAAAGAGC 9458  
Qy 3601 ACCCAGGACTGTCTATATGGAAGAAAGACAGGAGTCAACTCACCCTTCACAAAATAGGGA 3660  
Db 9459 ACCCAGGACTGTCTATATGGAAGAAAGACAGGAGTCAACTCACCCTTCACAAAATAGGGA 9518  
Qy 3661 CCAGACACAGCTGATGGTATGAGTTGATGCAAGGTGTGGAGCCTCAACCTCTGCTCCC 3720  
Db 9519 CCAGACACAGCTGATGGTATGAGTTGATGCAAGGTGTGGAGCCTCAACCTCTGCTCCC 9578  
Qy 3721 CTCCTACTACACATGGTTAAGCCCTGTGCTCTGTCTCAGGTTACACTCTCTGCACTA 3780  
Db 9579 CTCCTACTACACATGGTTAAGCCCTGTGCTCTGTCTCAGGTTTACACTCTCTGCACTA 9638  
Qy 3781 CCTCTTCATGGTGCCTCAGACGAGCACTTGGTCTTTCTTGTGTTGAAGCTTTGGGCTA 3840  
Db 9639 CCTCTTCATGGTGCCTCAGACGAGCACTTGGTCTTTCTTGTGTTGAAGCTTTGGGCTA 9698  
Qy 3841 CGTGATGACCAAGCTGTTTCTGTCTATGATCATGAGAGTGCCTGTGGAGCCCCGAAC 3900  
Db 9699 CRTGATGACCAAGCTGTTTCTGTCTATGATCATGAGAGTGCCTGTGGAGCCCCGAAC 9758  
Qy 3901 TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAAGTCTGAA 3960  
Db 9759 TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAAGTCTGAA 9818  
Qy 3961 AGGTGGGATCACATGTTTCACTGTTGACTTCTGGAATATTATGGAATATCAACACAG 4020  
Db 9819 ASGTGGGATCACATGTTTCACTGTTGACTTCTGGAATATTATGGAATATCAACACAG 9878  
Qy 4021 CAAGGATATGGAGAGGGGCTCACCTTCTGAGGTTGTGAGAGCTTTTCACTTTTC 4080  
Db 9879 CAAGGATATGGAGAGGGGCTCACCTTCTGAGGTTGTGAGAGCTTTTCACTTTTC 9938  
Qy 4081 ATGCATCTTGAAGAAACAGCTGGAGTCTGAGTCTTGTGGAGCAGGAGAGGGAAG 4140  
Db 9939 ATGCATCTTGAAGAAACAGCTGGAGTCTGAGTCTTGTGGAGCAGGAGAGGGAAG 9998  
Qy 4141 GAAATTTGCTTCTGAGATCATTTGGTCTTGGGATGGTGGAAATAGGGAATTTCTT 4200  
Db 9999 GAAATTTGCTTCTGAGATCATTTGGTCTTGGGATGGTGGAAATAGGGAATTTCTT 10058  
Qy 4201 TGGTTGCAAGTTAAAGGCTGGGATTTTCCAGAGTCCCAACCCCTCAGGTCACTCTG 4260  
Db 10059 TGGTTGCAAGTTAAAGGCTGGGATTTTCCAGAGTCCCAACCCCTCAGGTCACTCTG 10118  
Qy 4261 GGCTGTGAATGCAAGAGACAAAGTACCAGGCTACTGGAAGTACGGGTATGATGG 4320  
Db 10119 GGCTGTGAATGCAAGAGACAAAGTACCAGGCTACTGGAAGTACGGGTATGATGG 10178  
Qy 4321 CAGGACCACTTGAATTTCTGCCCTGCACACCTGGAATGGAGCAGCAGAAACCCAGGGCC 4380  
Db 10179 CAGGACCACTTGAATTTCTGCCCTGCACACCTGGAATGGAGCAGCAGAAACCCAGGGCC 10238  
Qy 4381 TGGCCCAACCAAGCTGAGTGGGAAGGACAAAGATTCGGGCCAGGACAAACAGGCTTAC 4440  
Db 10239 TGGCCCAACCAAGCTGAGTGGGAAGGACAAAGATTCGGGCCAGGACAAACAGGCTTAC 10298  
Qy 4441 CTGGAGAGGACTGCCCTGCACAGCTGCAGAGTGTCTGGAGCTGGGAGAGGTTTTC 4500  
Db 10299 CTGGAGAGGACTGCCCTGCACAGCTGCAGAGTGTCTGGAGCTGGGAGAGGTTTTC 10358  
Qy 4501 GACCAACAAGGTATGGTGGAAACACATTTCTGCCCTTACTCTAGTGGCAGAGTGGAGG 4560  
|||||

Db 10359 GACCAACAAGGTATGGTGGAAACACACTTCTGCCCTTATATCTAGTGGCAGAGTGGAGG 10418  
Qy 4561 AGGTTGACAGGCAACGGAATCCCTGGTTGGAGTTTCAAGAGTGGCTGAGGCTGTGTGCTTC 4620  
Db 10419 AGGTTGACAGGCAACGGAATCCCTGGTTGGAGTTTCAAGAGTGGCTGAGGCTGTGTGCTTC 10478  
Qy 4621 TCCAAATTTCTGGGAAGGAGCTTTCTCAATCTAGAGTCTCTACCTTATAATTTAGATCTA 4680  
Db 10479 TCCAAATTTCTGGGAAGGAGCTTTCTCAATCTAGAGTCTCTACCTTATAATTTAGATCTA 10538  
Qy 4681 TGAGACAGCCACAAAGTCAATGGTTTAAATTTCTTTTCTCATGCATATGGCTCAAAGGAA 4740  
Db 10539 TGAGACAGCCACAAAGTCAATGGTTTAAATTTCTTTTCTCATGCATATGGCTCAAAGGAA 10598  
Qy 4741 GTGTCTATGGCCCTTGTCTTTTATTAACCAATTAATCTTTTGTATATTTATACCTGTAA 4800  
Db 10599 GTGTCTATGGCCCTTGTCTTTTATTAACCAATTAATCTTTTGTATATTTATACCTGTAA 10658  
Qy 4801 AAATTCAGAAATGTCAAGCCGGCCGACGGTGGCTCACCCCTGTAATCCAGCACTTTGGG 4860  
Db 10659 AAATTCAGAAATGTCAAGCCGGCCGACGGTGGCTCACCCCTGTAATCCAGCACTTTGGG 10718  
Qy 4861 AGGCCGAGGGGGTGGTCAAAAGGTCAAGAGTTCAGAGTTCAGACAGCCTGACCAACATGGTGAA 4920  
Db 10719 AGKCGAGGGGGTGGTCAAAAGGTCAAGAGTTCAGAGTTCAGACAGCCTGACCAACATGGTGAA 10778  
Qy 4921 ACCCGTCTCTAAAAAATACAAAAATTAAGTGGTTCAGAGTTCAGAGTTCAGAGCCTGTGTAGTCCA 4980  
Db 10779 ACCCGTCTCTAAAAAATACAAAAATTAAGTGGTTCAGAGTTCAGAGTTCAGAGCCTGTGTAGTCCA 10838  
Qy 4981 GCTAATTTGGAAGGCTGAGGC 5000  
Db 10839 GCTAATTTGGAAGGCTGAGGC 10858

RESULT 8

US-10-301-844-2/c  
; Sequence 2, Application US/10301844  
; Publication No. US20030100747A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruddy, David A.  
; ; Wolff, Roger K.  
; ;  
; TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN  
; ;  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds, LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; FILING DATE: 20-No. US20030100747A1-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/852,495C  
; FILING DATE: 07-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Poissant, Brian M  
; REGISTRATION NUMBER: 28,462  
; REFERENCE/DOCKET NUMBER: 8907-0057-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 2:



## SEQUENCE CHARACTERISTICS:

LENGTH: 237326 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-301-844-2

## Query Match

99.2%; Score 4958.8; DB 15; Length 237326;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 4996; Conservative 0; Mismatches 2; Indels 6; Gaps 3;

QY	1	TCTAAGGTTGAGATAAAATTTTAAATGTATGATGAAATTTTGAATAATCATAAATATTTA	60
DB	47101	TCTAAGGTTGAGATAAAATTTTAAATGTATGATGAAATTTTGAATAATCATAAATATTTA	47042
QY	61	AATATCTAAGTTTCAGATCAGACATTTGCGAGCTACTTTTCCCAATCAACAACCCCT	120
DB	47041	AATATCTAAGTTTCAGATCAGACATTTGCGAAGCTACTTTTCCCAATCAACAACCCCT	46982
QY	121	TCAGGATTTAAACCAAGGGGACACTGGATCACCTAGTGTTCACAAGCAGGTACCTT	180
DB	46981	TCAGGATTTAAACCAAGGGGACACTGGATCACCTAGTGTTCACAAGCAGGTACCTT	46922
QY	181	CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTGCTTTTCCACGAGAGTT	240
DB	46921	CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTGCTTTTCCACGAGAGTT	46862
QY	241	TTACTGGGCATCTCTGAGCCTAGGCAATAGCTGTAGGCTGACTCTGAGGCATCCCG	300
DB	46861	TTACTGGGCATCTCTGAGCCTAGGCAATAGCTGTAGGCTGACTCTCTGGAGCCATCCCG	46802
QY	301	TTTCCCGCCGCCCAAGAGCGGAGATTTAAACGGGGACGTGCGGCCAGAGCTGGGGAA	360
DB	46801	TTTCCCGCCGCCCAAGAGCGGAGATTTAAACGGGGACGTGCGGCCAGAGCTGGGGAA	46742
QY	361	ATGGGCCCGCAGCCAGCCGCGCTTCTCCTCTGATGCTTTTGCAGACCGCGTCTTG	420
DB	46741	ATGGGCCCGCAGCCAGCCGCGCTTCTCCTCTGATGCTTTTGCAGACCGCGTCTTG	46682
QY	421	CAGGGCGCTTCTGCTGCTGAGTCCGAGGCTCGGGCGAACTAGGGGCGCGCGGGGTG	480
DB	46681	CAGGGCGCTTCTGCTGCTGAGTCCGAGGCTCGGGCGAACTAGGGGCGCGCGGGGTG	46622
QY	481	GAATAATCGAAACTAGCTTTTCTTTGCGCTTGGAGTTTGCTTAATTTTGAGAGCACTGC	540
DB	46621	GAATAATCGAAACTAGCTTTTCTTTGCGCTTGGAGTTTGCTTAATTTTGAGAGCACTGC	46562
QY	541	TCACCCCTATCCGCAAGCCCTCTCCCTACTTTTCTGCTGCTCAGACCCCGTGAGGGAGTGC	600
DB	46561	TCACCCCTATCCGCAAGCCCTCTCCCTACTTTTCTGCTGCTCAGACCCCGTGAGGGAGTGC	46502
QY	601	CTACCACTGAACTGAGAGTGGGTCTTGGCCCGCAGACCTGCGCCCTCCCGCGGTGT	660
DB	46501	CTACCACTGAACTGAGAGTGGGTCTTGGCCCGCAGACCTGCGCCCTCCCGCGGTGT	46442
QY	661	CCCGGCTCTGCGAGTGACTTTTGGAAACCGCCACTTCCCTTCCCGCAACTAGAAATGCTTT	720
DB	46441	CCCGGCTCTGCGAGTGACTTTTGGAAACCGCCACTTCCCTTCCCGCAACTAGAAATGCTTT	46382
QY	721	TAAATAAATCTCGTAGTCTCTCACTGAGCTGAGCTTAAGCCTGGGGCTCTTTGAACCTGG	780
DB	46381	TAAATAAATCTCGTAGTCTCTCACTGAGCTGAGCTTAAGCCTGGGGCTCTTTGAACCTGG	46322
QY	781	AACTCGGGTTATTTTCAATGTGAGTGTGAGTTTTCCTCCAGTCACTCTCAACACAGG	840
DB	46321	AACTCGGGTTATTTTCAATGTGAGTGTGAGTTTTCCTCCAGTCACTCTCTCAACACAGG	46262
QY	841	AAAGTTCTCCCTGAGTGTGTCGAGAGAGGCTGAGCAACCCACACAGCAGGATCCGACGG	900
DB	46261	AAAGTTCTCCCTGAGTGTGTCGAGAGAGGCTGAGCAACCCACACAGCAGGATCCGACGG	46202
QY	901	GGTTTCCACCTCAGAACGAAATGCGTTGGGCGGTGGGGCGCGAAGAGTGGGCTTGGGGA	960

DB	46201	GGTTTCCACCTCAGAACGAATGCGTTGGCGGTGGGGCGCGAAGAGTGGGCTTGGGGA	46142
QY	961	TCTGAATTTCTTCCACCATTTCCACCCACTTTTGGTGAGAGCTGGGGTGAGGCTCTTAGGGT	1020
DB	46141	TCTGAATTTCTTCCACCATTTCCACCCACTTTTGGTGAGAGCTGGGGTGAGGCTCTTAGGGT	46082
QY	1021	GGGAGGCTCTGAGAGAGGCTTACCTCGGGCTTTTCCCACTCTTTGGCAATTTGTTCTTTT	1080
DB	46081	GGGAGGCTCTGAGAGAGGCTTACCTCGGGCTTTTCCCACTCTTTGGCAATTTGTTCTTTT	46022
QY	1081	GCTCGAAAAATTAAGTATATGTTAGTTTGAACGTTTGAACAAATTTCTCTTTTCGG	1140
DB	46021	GCTCGAAAAATTAAGTATATGTTAGTTTGAACGTTTGAACAAATTTCTCTTTTCGG	45962
QY	1141	CTAGGCTTTATGATTTGCAATGCTGTAATTAAGAGGCTCTCTCAAAAGTACTGA	1200
DB	45961	CTAGGCTTTATGATTTGCAATGCTGTAATTAAGAGGCTCTCTCAAAAGTACTGA	45902
QY	1201	TAATGAACATGTAAGCAATGCACTCACTTCTAAGTTTACATTCATATCTGATCTTATTGA	1260
DB	45901	TAATGAACATGTAAGCAATGCACTCACTTCTAAGTTTACATTCATATCTGATCTTATTGA	45842
QY	1261	TTTTCACTAGGCATAGGAGGTAGAGCTTAATAACGTTTATTTTACTAGAAGTTAACT	1320
DB	45841	TTTTCACTAGGCATAGGAGGTAGAGCTTAATAACGTTTATTTTACTAGAAGTTAACT	45782
QY	1321	GGAAATTCAGATTTATTAATCTTTTCAAGTTTCAAAAGAACATAAATATCTGGTTCTTG	1380
DB	45781	GGAAATTCAGATTTATTAATCTTTTCAAGTTTCAAAAGAACATAAATATCTGGTTCTTG	45722
QY	1381	ATGTTATTTTCAAGTACTACAGCTGTTCTAATCTTGTAGTGACGATTTTCCCTCTGAG	1440
DB	45721	ATGTTATTTTCAAGTACTACAGCTGTTCTAATCTTGTAGTGACGATTTTCCCTCTGAG	45662
QY	1441	TGTAGCAGAGTCTTCTGTGGGTCAACCGCGGCTTCAGCACAGCACTTTGAGTTTGTGA	1500
DB	45661	TGTAGCAGAGTCTTCTGTGGGTCAACCGCGGCTTCAGCACAGCACTTTGAGTTTGTGA	45602
QY	1501	CTACGCTGATCCACATTTTACATGACAAAGTACGAGCAGTGGCAGGCTCTTCTCTG	1560
DB	45601	CTACGCTGATCCACATTTTACATGACAAAGTACGAGCAGTGGCAGGCTCTTCTCTG	45542
QY	1561	CAAAATTTTCAATGCTACATCGGCTTTGGTGGCAGAGCTCATGCTCTCACTTCATAGC	1620
DB	45541	CAAAATTTTCAATGCTACATCGGCTTTGGTGGCAGAGCTCATGCTCTCACTTCATAGC	45482
QY	1621	TATGATTTCTTAAACATCACTGCAATTAGAGTTGAATAAATAAATTTCACTGTTGAGCAG	1680
DB	45481	TATGATTTCTTAAACATCACTGCAATTAGAGTTGAATAAATAAATTTCACTGTTGAGCAG	45422
QY	1681	AAATATTTCTTTTACAAAGTGAATGAGTCCAGCCATGTTGTCATCTGTTCAAGCCC	1740
DB	45421	AAATATTTCTTTTACAAAGTGAATGAGTCCAGCCATGTTGTCATCTGTTCAAGCCC	45362
QY	1741	CAAGGAGAGAGCAGGAGAAACAAGTCTTTTACCTTTTGTATTTTGCATTTCTAGTGGAGA	1800
DB	45361	CAAGGAGAGAGCAGGAGAAACAAGTCTTTTACCTTTTGTATTTTGCATTTCTAGTGGAGA	45302
QY	1801	GATGCAATAAGCAAAATGAGCAGAAAGATATACAACTACAGGAAATCATGGGTGTTGA	1860
DB	45301	GATGCAATAAGCAAAATGAGCAGAAAGATATACAACTACAGGAAATCATGGGTGTTGA	45242
QY	1861	GAACGAGAGAGTCAAGGCAAGTCACTCTGGGCTGACACTTGAACAGACATCAAGGA	1920
DB	45241	GAACGAGAGAGTCAAGGCAAGTCACTCTGGGCTGACACTTGAACAGACATCAAGGA	45182
QY	1921	AATAAGATGATATTTGACTGGAGCAGTATTTTCCAGCAAACTGAGTGGGCTCTGGCAAG	1980
DB	45181	AATAAGATGATATTTGACTGGAGCAGTATTTTCCAGCAAACTGAGTGGGCTCTGGCAAG	45122
QY	1981	TTGATTTAAAGCGGGTTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGGG	2040



45121	TTGGATTAAAGAGCGGGTTTCTCAGCACTACTCATGTGTGTGTGTGT- GGCGGGGGGGGG	45063
2041	CGGCGTGGGGGTGGGAAGGGGCACTACCATCTGCATGTAGGATGTCTAGCAGTATCCTGT	2100
45062	CGGCGTGGGGGTGGGAAGGGGCACTACCATCTGCATGTAGGATGTCTAGCAGTATCCTGT	45003
2101	CCTCCCTACTCATCTAGTGTCTAGGAGCACTCCCCAGTCTTGACAAACCAAAATCTCTCT	2160
45002	CCTCCCTACTCATCTAGTGTCTAGGAGCACTCCCCAGTCTTGACAAACCAAAATCTCTCT	44943
2161	AAACTTTGGCCACATGTCACCTAGTAGACAAATCTCTGGTTAGAGCTCGGGTTGAAAA	2220
44942	AAACTTTGGCCACATGTCACCTAGTAGACAAATCTCTGGTTAGAGCTCGGGTTGAAAA	44883
2221	AATAAACAACTAGTGTCTGGGAGTTAGAGGCCAAGAACTAGTAAATGGGCTCAGAAGAGA	2280
44882	AATAAACAACTAGTGTCTGGGAGTTAGAGGCCAAGAACTAGTAAATGGGCTCAGAAGAGA	44823
2281	GCCACAAACAAAGTTGTGCAGGGCGCTGTAGGCTGTGGTGTGAAATTTCTAGCCCAAGGAT	2340
44822	GCCACAAACAAAGTTGTGCAGGGCGCTGTAGGCTGTGGTGTGAAATTTCTAGCCCAAGGAT	44763
2341	ACAGTGATCTGTACAGGCTTTTAAAGATTGCTCTGGCTGTACTATGTGGAAGACGAATG	2400
44762	ACAGTGATCTGTACAGGCTTTTAAAGATTGCTCTGGCTGTACTATGTGGAAGACGAATG	44703
2401	AAGGGAGCAACAGTAAAGCAGGGAGGCCAGCCAGCAAGCTGTTCACAGTCCAGGCAAG	2460
44702	AAGGGAGCAACAGTAAAGCAGGGAGGCCAGCCAGCAAGCTGTTCACAGTCCAGGCAAG	44643
2461	AGGTAGTGGAGTGGGCTGGGTGGGAAACAGAAAAAGGAGTGACAAAAACCAATTTGCTCTGAA	2520
44642	AGGTAGTGGAGTGGGCTGGGTGGGAAACAGAAAAAGGAGTGACAAAAACCAATTTGCTCTGAA	44583
2521	TATATTTCTGAAGGAAGTTGCTGGAAGGATTTCTATGTTGTGTGTGTGTGTGTGTGTGTGT	2580
44582	TATATTTCTGAAGGAAGTTGCTGGAAGGATTTCTATGTTGTGTGTGTGTGTGTGTGTGTGT	44523
2581	CTGGGTGTAGTACGTCAATGCCAAGGAGGAGGCCAAGCAGAGCAGATTTCTCTGAGCTCAGGA	2640
44522	CTGGGTGTAGTACGTCAATGCCAAGGAGGAGGCCAAGCAGAGCAGATTTCTCTGAGCTCAGGA	44463
2641	GTTTCAAGACCAAGCCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAATACAAAAAATTA	2700
44462	GTTTCAAGACCAAGCCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAATACAAAAAATTA	44403
2701	GCTGGGTGTGTGTGTCATGCACTGTGTGATCTCTGAGTACTCGGAGAGGCTGAGGTGTGAGGTA	2760
44402	GCTGGGTGTGTGTGTCATGCACTGTGTGATCTCTGAGTACTCGGAGAGGCTGAGGTGTGAGGTA	44343
2761	TTGTCTGAGCCCAAGAAAGTTGAGGCTGAGTGTGAGCCATGATGTGCACTGTACTTTACG	2820
44342	TTGTCTGAGCCCAAGAAAGTTGAGGCTGAGTGTGAGCCATGATGTGCACTGTACTTTACG	44283
2821	CTAGGTGACAGAGCAAGACCCCTGCTCCCCCTGACCCCTGAAAAAGAGAGTTTAAAGT	2880
44282	CTAGGTGACAGAGCAAGACCCCTGCTCCCCCTGACCCCTGAAAAAGAGAGTTTAAAGT	44223
2881	TGACTTTGTCTTTATTTTATTTTATTTATTTGTCCTGTAGCAGTGGGGTAAATTTGGCAATGCCAT	2940
44222	TGACTTTGTCTTTATTTTATTTTATTTTATTTGTCCTGTAGCAGTGGGGTAAATTTGGCAATGCCAT	44163
2941	TTCTGTAGATGGTGAAGGCACAGAGAAAGACAGTTTGGGGTAAATCAAGGATCTGCATTTTG	3000
44162	TTCTGTAGATGGTGAAGGCACAGAGAAAGACAGTTTGGGGTAAATCAAGGATCTGCATTTTG	44104
3001	GGACATGTTAAGTTTGTAGATTTCCAGTCAGGCTTTCCAAAGTGGTGTGAGGCCACATAGGCAGTT	3060
44103	GGACATGTTAAGTTTGTAGATTTCCAGTCAGGCTTTCCAAAGTGGTGTGAGGCCACATAGGCAGTT	44044
3061	CAGTGTGAAGAAATTCAGGACCAAGGCTGGGCAACGGTGGCTCACTTCTGTAAATCCCAAGCACT	3120
44043	CAGTGTGAAGAAATTCAGGACCAAGGCTGGGCAACGGTGGCTCACTTCTGTAAATCCCAAGCACT	43984

QY	3121	TTGGTGGCTGAGCGAGTGAATCATTTGAGGTGAGAGTTTGAGCAAGCTTTGGCCAACA	3180
DB	43983	TTGGTGGCTGAGCGAGTGAATCATTTGAGGTGAGAGTTTGAGCAAGCTTTGGCCAACA	43920
QY	3181	TGGTGAACCCCATGCTCTACTAAAAATACAAAAATTTAGCCTGGTGGTGGCGCAGCCT	3240
DB	43923	TGGTGAACCCCATGCTCTACTAAAAATACAAAAATTTAGCCTGGTGGTGGCGCAGCCT	43866
QY	3241	ATAGTCCACAGTTTTCAGGAGGCTTAGGTAGGAGAACTCCCTTGAACCCAGGAGGTGCAGG	3300
DB	43863	ATAGTCCACAGTTTTCAGGAGGCTTAGGTAGGAGAACTCCCTTGAACCCAGGAGGTGCAGG	43804
QY	3301	TTGCAGGTGAGCTGAGATTGTGCCACTGCACCTCCAGCCTCGGGTGATAGAGTGAGACTCTGT	3360
DB	43803	TTGCAGGTGAGCTGAGATTGTGCCACTGCACCTCCAGCCTCGGGTGATAGAGTGAGACTCTGT	43744
QY	3361	CTC-----AA	3416
DB	43743	CTCAAA	43684
QY	3417	TGGGTCTAAATTTGCCCTGAGCACAACTCCTGAGTTCAACTACCATGGCTAGACACACCT	3476
DB	43683	TGGGTCTAAATTTGCCCTGAGCACAACTCCTGAGTTCAACTACCATGGCTAGACACACCT	43624
QY	3477	TAAACATTTTCTGAATCCACAGCTTTTAGTGGAGTCTGTCTAATCATAGATATTGGAATA	3536
DB	43623	TAAACATTTTCTGAATCCACAGCTTTTAGTGGAGTCTGTCTAATCATAGATATTGGAATA	43564
QY	3537	GGAATCTGGGGGAGTCAGGGGGTGGCAGCCACTGTGTGGCAGAGAAAGCACAAAGGAAA	3596
DB	43563	GGAATCTGGGGGAGTCAGGGGGTGGCAGCCACTGTGTGGCAGAGAAAGCACAAAGGAAA	43504
QY	3597	GAGCACCCAGGACTGTCTATATGGAAGAAAGACAGGACTGCAACTCACCCCTTCACAAAATG	3656
DB	43503	GAGCACCCAGGACTGTCTATATGGAAGAAAGACAGGACTGCAACTCACCCCTTCACAAAATG	43444
QY	3657	AGGACACAGACACAGCTGATGTTATGATGTGATGCAGGTGTGTGGAGCTTCAACATCCTGC	3716
DB	43443	AGGACACAGACACAGCTGATGTTATGATGTGATGCAGGTGTGTGGAGCTTCAACATCCTGC	43384
QY	3717	TCCCTCCTACTACACATGGTTAAGCCCTGTTGCTCTGTCTCCAGGTTCAACATCCTGC	3776
DB	43383	TCCCTCCTACTACACATGGTTAAGCCCTGTTGCTCTGTCTCCAGGTTCAACATCCTGC	43324
QY	3777	ACTACCTCTTCATGGGTGCTCAGACAGGACTTGGTCTTTCTTTTGAAGCTTTGG	3836
DB	43323	ACTACCTCTTCATGGGTGCTCAGACAGGACTTGGTCTTTCTTTTGAAGCTTTGG	43264
QY	3837	GCTACGTGGATACAGCTGTTCTGTCTCTATGATCATGAGAGTCGCGGTGGAGCCCC	3896
DB	43263	GCTACGTGGATACAGCTGTTCTGTCTCTATGATCATGAGAGTCGCGGTGGAGCCCC	43204
QY	3897	GAATCCATCGGTTTCCAGTAGAAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTC	3956
DB	43203	GAATCCATCGGTTTCCAGTAGAAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAGAGTC	43144
QY	3957	TGAAAGGGTGGGATCACATGTTCACTGTGGACTTTCTGGACTATTATGGAATAATCAACCC	4016
DB	43143	TGAAAGGGTGGGATCACATGTTCACTGTGGACTTTCTGGACTATTATGGAATAATCAACCC	43084
QY	4017	ACAGCAGGGTATGCGAGAGGGGGCTCACCTTCTGAGGTTGTTCAGAGCTTTTCATCT	4076
DB	43083	ACAGCAGGGTATGCGAGAGGGGGCTCACCTTCTGAGGTTGTTCAGAGCTTTTCATCT	43024
QY	4077	TTTTCATGCATCTTTGAAGGAAACAGCTGGAAGTCTGAGGCTTGTGGGACAGGGAAGAGG	4136
DB	43023	TTTTCATGCATCTTTGAAGGAAACAGCTGGAAGTCTGAGGCTTGTGGGACAGGGAAGAGG	42964
QY	4137	GAAGGAAATTTGCTTCTTGATATCAATTTGGTCTTGGGATGGTGGNAATAGGACCTATT	4196
DB	42963	GAAGGAAATTTGCTTCTTGATATCAATTTGGTCTTGGGATGGTGGNAATAGGACCTATT	42904



QY 4197 CTTTGGTGTGAGTAAACAGGCTGGGATTTTTCCAGAGTCCACACCTCGAGTCAAT 4256  
DB CTTTGGTGTGAGTAAACAGGCTGGGATTTTTCCAGAGTCCACACCTCGAGTCAAT 42844  
QY 4257 CTTGGGCTGTGAATACCAAGACACAGTACCGAGGCTACTGGAAGTACGGGTATGA 4316  
DB CTTGGGCTGTGAATACCAAGACACAGTACCGAGGCTACTGGAAGTACGGGTATGA 42784  
QY 4317 TGGGACAGGACCACTTTGAAATTTGCGCTTGACACACCTGGGATTTGAGAGCAGCAACCCAG 4376  
DB TGGGACAGGACCACTTTGAAATTTGCGCTTGACACACCTGGGATTTGAGAGCAGCAACCCAG 42724  
QY 4377 GGCCTGCCCAACAAGCTGAGTGGGAAAGGCAACAAGATTGGGCCAGGACAGGCG 4436  
DB GGCCTGCCCAACAAGCTGAGTGGGAAAGGCAACAAGATTGGGCCAGGACAGGCG 42664  
QY 4437 CTACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTGTGCTGGAGCTGGGAGAGGTGT 4496  
DB CTACCTGGAGAGGAGCTGCCCTGCACAGCTGCAGCAGTGTGCTGGAGCTGGGAGAGGTGT 42604  
QY 4497 TTTGGACCAACAGGATATGGTGGAAACACACTTCTGCCCTATACCTAGTGGCAGAGTG 4556  
DB TTTGGACCAACAGGATATGGTGGAAACACACTTCTGCCCTATACCTAGTGGCAGAGTG 42544  
QY 4557 GAGGAGGTTGCAGGGCACCGAAATCCCTGGTGGAGTTTCAGAGTGGCTGAGGCTGTGTG 4616  
DB GAGGAGGTTGCAGGGCACCGAAATCCCTGGTGGAGTTTCAGAGTGGCTGAGGCTGTGTG 42484  
QY 4617 CCTCTCCAAATTCGGGAAGGACCTTCTCAATCCTAGAGTCTCTACCTTAAATTGAGA 4676  
DB CCTCTCCAAATTCGGGAAGGACCTTCTCAATCCTAGAGTCTCTACCTTAAATTGAGA 42424  
QY 4677 TGTATGAGACAGCCAAAGTCATGGGTTAAATTTCTTCTCATGCTATGGCTCAAG 4736  
DB TGTATGAGACAGCCAAAGTCATGGGTTAAATTTCTTCTCATGCTATGGCTCAAG 42304  
QY 4797 TTAATAATTCAGAAATGTCAAGCCGGGACCGTGGCTCACCCCTGTAAATCCAGACTT 4856  
DB TTAATAATTCAGAAATGTCAAGCCGGGACCGTGGCTCACCCCTGTAAATCCAGACTT 42244  
QY 4857 TGGGAGGCGGAGCGGCTGGTCAAGAGTCAGAGTTTCAGAGCAGCCTGACCAACATGG 4916  
DB TGGGAGGCGGAGCGGCTGGTCAAGAGTCAGAGTTTCAGAGCAGCCTGACCAACATGG 42184  
QY 4917 TGAAACCCGCTCTTAAAAAATACAAAAATTAGCTGGTCAAGTCAATGCGCACTGTAGT 4976  
DB TGAAACCCGCTCTTAAAAAATACAAAAATTAGCTGGTCAAGTCAATGCGCACTGTAGT 42124  
QY 4977 CCCAGCTAATTCGAAGGCTGAGGC 5000  
DB CCCAGCTAATTCGAAGGCTGAGGC 42100

RESULT 9  
US-09-981-606-27  
; Sequence 27, Application US/09981606  
; Publication NO. US20030129595A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothenberg et al.  
; TITLE OF INVENTION: Mutations associated with iron disorders  
; FILE REFERENCE: 24065-004CON  
; CURRENT APPLICATION NUMBER: US/09/981,606  
; CURRENT FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 09/277,457  
; PRIOR FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 12146

; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-981-606-27  
Query Match 99.1%; Score 4957.2; DB 10; Length 12146;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 4995; Conservative 0; Mismatches 3; Indels 6; Gaps 3;  
QY 1 TCTAAGTTGAGATATAATTTTAAATGTATGATTTGAAATCATATAATATTTA 60  
DB TCTAAGTTGAGATATAATTTTAAATGTATGATTTGAAATCATATAATATTTA 948  
QY 61 AATATCTAAAGTTTCAGATCAGAACATTTGCGAAGCTACTTTTCCCAATCAACACCCCT 120  
DB AATATCTAAAGTTTCAGATCAGAACATTTGCGAAGCTACTTTTCCCAATCAACACCCCT 1008  
QY 121 TCAGGATTTAAATAACCAAGGGGGAACCTGGATCACTAGTGTTCACAGAGGATACCTT 180  
DB TCAGGATTTAAATAACCAAGGGGGAACCTGGATCACTAGTGTTCACAGAGGATACCTT 180  
QY 1009 TCAGGATTTAAATAACCAAGGGGGAACCTGGATCACTAGTGTTCACAGAGGATACCTT 1068  
DB TCAGGATTTAAATAACCAAGGGGGAACCTGGATCACTAGTGTTCACAGAGGATACCTT 1068  
QY 181 CTGCTGTAGGAGAGAGAGAACTAAAGTTCTGAAAGACCTGTGTGCTTTTCCACGAGGAT 240  
DB CTGCTGTAGGAGAGAGAGAACTAAAGTTCTGAAAGACCTGTGTGCTTTTCCACGAGGAT 1128  
QY 241 TTAATGGGATCTCCTGAGCCTAGGCAATAGCTGTAGGCTGACTTCTGGAGCCATCCCCG 300  
DB TTAATGGGATCTCCTGAGCCTAGGCAATAGCTGTAGGCTGACTTCTGGAGCCATCCCCG 1188  
QY 301 TTTCCCGCGCCCCCAAAAGAGCGGAGATTTAAACGGGGAAGTTCGGCCAGAGCTGGGAA 360  
DB TTTCCCGCGCCCCCAAAAGAGCGGAGATTTAAACGGGGAAGTTCGGCCAGAGCTGGGAA 1248  
QY 361 ATGGCCCGCGCAGCAGCGCGCTCTCTCTCTGATGCTTTTGAGAGCCGCGGCTCTG 420  
DB ATGGCCCGCGCAGCAGCGCGCTCTCTCTCTGATGCTTTTGAGAGCCGCGGCTCTG 1308  
QY 421 CAGGGGCGCTTCTGCTGCTGAGTCCGAGGCTCGCGGCGAACTAGGGGCGCGCGGGGTG 480  
DB CAGGGGCGCTTCTGCTGCTGAGTCCGAGGCTCGCGGCGAACTAGGGGCGCGCGGGGTG 1368  
QY 481 GAAAAATCGAAATAGCTATTTTCTTGGCTTTGGGAGTTTGTCTAACTTTGGAGGACCTGC 540  
DB GAAAAATCGAAATAGCTATTTTCTTGGCTTTGGGAGTTTGTCTAACTTTGGAGGACCTGC 1428  
QY 541 TCAACCTCTATCCGAAAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600  
DB TCAACCTCTATCCGAAAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1488  
QY 601 CTACCACTGAACTGAGATAGGGGTCTCTCGCCCGAGGACCTGCGCCCTCTCTCTCTCTCT 660  
DB CTACCACTGAACTGAGATAGGGGTCTCTCGCCCGAGGACCTGCGCCCTCTCTCTCTCTCT 1548  
QY 661 CCGGCTCTGGGAGTGAATTTTGGAAACCGGCCACTCCCTTCTCTCTCTCTCTCTCTCTCT 720  
DB CCGGCTCTGGGAGTGAATTTTGGAAACCGGCCACTCCCTTCTCTCTCTCTCTCTCTCTCT 1608  
QY 721 TAAATAAATCTGATTTCTCAATGTGAGTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 780  
DB TAAATAAATCTGATTTCTCAATGTGAGTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1668  
QY 781 AACTCGGGTTTATTTTCAATGTGAGTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840  
DB AACTCGGGTTTATTTTCAATGTGAGTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1728  
QY 841 AAGTTCTTCTCTGAGTGTTCGCGAGAGGCTGAGCAAAACCCACAGCAGGATCCGACGG 900  
DB AAGTTCTTCTCTGAGTGTTCGCGAGAGGCTGAGCAAAACCCACAGCAGGATCCGACGG 1788  
QY 901 GGTTCACCTCAGAACGAATGCGTGGGCGGCGGAGAGTGGGTTGGGA 960  
DB GGTTCACCTCAGAACGAATGCGTGGGCGGCGGAGAGTGGGTTGGGA 960  
QY 961 TCTGAATTTCTTCAACCTTCCACCCACTTTTGTGTAGACCTGGGGTGGAGGTCTCTAGGT 1020



1849	Db	 TCTGAATTCCTTCACCAATTCACCCACTTTTGGTGAGACCTTGGGGTGAGGTCTCTAGGGT	1908
1021	Qy	GGGAGGCTCCTGAGAGAGGCTACTCTCGGGCCCTTCCCCCACTCTTGGCAATTTGTTCTTTTT	1080
1909	Db	GGGAGGCTCCTGAGAGAGGCTACTCTCGGGCCCTTCCCCCACTCTTGGCAATTTGTTCTTTTT	1968
1081	Qy	GCCTGGAAAAATAAGTATATGTTAGTTTGTGAACTGTTTGAACGTGAACAAATCTCTTTTCGG	1140
1969	Db	GCCTGGAAAAATAAGTATATGTTAGTTTGTGAACTGTTTGAACGTGAACAAATCTCTTTTCGG	2028
1141	Qy	CTAGGCTTTTATGATTTTGCAATGTGCTGTGTAAATTAAGAGGCCCTCTCTACAAGTACTGA	1200
2029	Db	CTAGGCTTTTATGATTTTGCAATGTGCTGTGTAAATTAAGAGGCCCTCTCTACAAGTACTGA	2088
1201	Qy	TAATGAACATGTAAGCAATGACACTCACTCTTAAGGTACATTTCAATATCTGATCTTATTTTGA	1260
2089	Db	TAATGAACATGTAAGCAATGACACTCACTCTTAAGGTACATTTCAATATCTGATCTTATTTTGA	2148
1261	Qy	TTTTCACTAGGCATAGGAGGTAGGAGCTAATAATAGCTTTATTTTACTAGAAGTTAACT	1320
2149	Db	TTTTCACTAGGCATAGGAGGTAGGAGCTAATAATAGCTTTATTTTACTAGAAGTTAACT	2208
1321	Qy	GGAAATTCAGATTTATTAACCTCTTTTCAGGTTTACAAGAAACATAAATAATCTGTTTTCTG	1380
2209	Db	GGAAATTCAGATTTATTAACCTCTTTTCAGGTTTACAAGAAACATAAATAATCTGTTTTCTG	2268
1381	Qy	ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTACGTTGACAGTGATTTTGCCCTGTAG	1440
2269	Db	ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTACGTTGACAGTGATTTTGCCCTGTAG	2328
1441	Qy	TGTAGCACAGTGTTCGTGGGTACACGCGGGCTCAGCACAGCACATTTTCAGATTTTGGTA	1500
2329	Db	TGTAGCACAGTGTTCGTGGGTACACGCGGGCTCAGCACAGCACATTTTCAGATTTTGGTA	2388
1501	Qy	CTACGTGTATCCACATTTTACATGAACAAGATAGGCCATGGCAACGCTGTCTTCTCTG	1560
2389	Db	CTACGTGTATCCACATTTTACATGAACAAGATAGGCCATGGCAACGCTGTCTTCTCTG	2448
1561	Qy	CAAAATTTTCAAGTGTACACTGGCTTTGGTGGCAGAGCTCATGTCTCCACATTCATAGC	1620
2449	Db	CAAAATTTTCAAGTGTACACTGGGGCTTTGGTGGCAGAGCTCATGTCTCCACATTCATAGC	2508
1621	Qy	TATGATTTCTTAAACATCACACTGATTTAGAGTTTGAATAATAAATTTTCAATGTAGCAG	1680
2509	Db	TATGATTTCTTAAACATCACACTGATTTAGAGTTTGAATAATAAATTTTCAATGTAGCAG	2568
1681	Qy	AAATATTTCTATGTTTACAAGTGTAAATGAGTCCAGCCATGTGTGCACTGTTTCAAGCCC	1740
2569	Db	AAATATTTCTATGTTTACAAGTGTAAATGAGTCCAGCCATGTGTGCACTGTTTCAAGCCC	2628
1741	Qy	CAAGGGAGAGACGAGGGAACAAGTCTTTTACCCTTTGATATTTTGCATTTCTAGTGGAGA	1800
2629	Db	CAAGGGAGAGACGAGGGAACAAGTCTTTTACCCTTTGATATTTTGCATTTCTAGTGGAGA	2688
1801	Qy	GATCACAAATAGCAAAATGACAGAGAAAGATATACAACATCAGGAAATCATGGGTGTTCTGA	1860
2689	Db	GATCACAAATAGCAAAATGACAGAGAAAGATATACAACATCAGGAAATCATGGGTGTTCTGA	2748
1861	Qy	GAAGCAGAGAAGTCAAGGCAAGTCACTCTCGGGCTGACACTTGTAGTGCAATCTAGTGGAGA	1920
2749	Db	GAAGCAGAGAAGTCAAGGCAAGTCACTCTCGGGCTGACACTTGTAGTGCAATCTAGTGGAGA	2808
1921	Qy	AATTAAGAAATGATATTTGACTGGGACAGTATTTTCCAGGCAAACTGAGTGGGCTGGCAAG	1980
2809	Db	AATTAAGAAATGATATTTGACTGGGACAGTATTTTCCAGGCAAACTGAGTGGGCTGGCAAG	2868
1981	Qy	TTTGATTTTAAAGCGGGTTTTTCTCAGACACTACTCATGTGTGTGTGTGTGTGTGTGTGTGT	2040
2869	Db	TTTGATTTTAAAGCGGGTTTTTCTCAGACACTACTCATGTGTGTGTGTGTGTGTGTGTGTGT	2927
2041	Qy	CGGCGTGGGGTGGGAAGGGGGACTACCATCTGCATGTAGGATGTCTAGCAGTATCTCTGT	2100

Db	2928	CGGCGTGGGGTGGGAAAGGGGGA	CTACCATCTCGATGTAGGATGTCTAGCAGTATCCTCT	2980
Qy	2101	CCTCCCTACTCACTAGGTGCTAGGAGCACTCC	CCCCAGTCTTTGACAACCAAAAAATGTCTCT	2160
Db	2988	CCTCCCTACTCACTAGGTGCTAGGAGCACTCC	CCCCAGTCTTTGACAACCAAAAAATGTCTCT	3047
Qy	2161	AAACTTTGCCACATGTCACTAGTAGACAAATC	CTCGTGTAAAGAGCTCGGTTGAAAAA	2220
Db	3048	AAACTTTGCCACATGTCACTAGTAGACAAATC	CTCGTGTAAAGAGCTCGGTTGAAAAA	3107
Qy	2221	AATAAACAAGTGTGCTGGGAGTAGAGGCCA	AGNAAGTAGGTAATGGGCTCAGAGGGA	2280
Db	3108	AATAAACAAGTGTGCTGGGAGTAGAGGCCA	AGNAAGTAGGTAATGGGCTCAGAGGGA	3167
Qy	2281	GCCACAAACAAGTTGTGCAGGCGCTGTAGGCT	GTGTGTAATCTAGCCAAAGAGTA	2340
Db	3168	GCCACAAACAAGTTGTGCAGGCGCTGTAGGCT	GTGTGTAATCTAGCCAAAGAGTA	3227
Qy	2341	ACAGTGATCTGTCA	CAGGCTTTTAAAGATTGCTCTGGCTGTATGTGGAACGCAATG	2400
Db	3228	ACAGTGATCTGTCA	CAGGCTTTTAAAGATTGCTCTGGCTGTATGTGGAACGCAATG	3287
Qy	2401	AAGGGACACAGTAAAGCAGGAGCC	CAGCCAGGAGAGCTGTACACAGTCCAGGCAAG	2460
Db	3288	AAGGGACACAGTAAAGCAGGAGCC	CAGCCAGGAGAGCTGTACACAGTCCAGGCAAG	3347
Qy	2461	AGGTAGTGAAGTGGGCTGGGATCGGAA	CAGAAAAAGGAGTGACAAAACATTTGCTCTCTGAA	2520
Db	3348	AGGTAGTGAAGTGGGCTGGGATCGGAA	CAGAAAAAGGAGTGACAAAACATTTGCTCTCTGAA	3407
Qy	2521	TATATTTCTGAAGAAAGTTGCTGAAGGATTC	TATGTTGTGAGAGAAAGAAATATGG	2580
Db	3408	TATATTTCTGAAGAAAGTTGCTGAAGGATTC	TATGTTGTGAGAGAAAGAAATATGG	3467
Qy	2581	CTGGGTGTAGTACTCATGCCAAGGAGGAGCC	CAAGGAGAGCAGATTCCTGAGCTCAGGA	2640
Db	3468	CTGGGTGTAGTACTCATGCCAAGGAGGAGCC	CAAGGAGAGCAGATTCCTGAGCTCAGGA	3527
Qy	2641	GTTCAAGACACAGCTGGGCAACACAGCAAAAC	CCCCCTTCTCTACAAAAATACAAAAATTA	2700
Db	3528	GTTCAAGACACAGCTGGGCAACACAGCAAAAC	CCCCCTTCTCTACAAAAATACAAAAATTA	3587
Qy	2701	GCTGGGTGTGGTGGCATGCA	CCCTGTGATCTAGCTACTCGGGAGGCTGAGGTGGAGGTA	2760
Db	3588	GCTGGGTGTGGTGGCATGCA	CCCTGTGATCTAGCTACTCGGGAGGCTGAGGTGGAGGTA	3647
Qy	2761	TTGCTTGAGCCCAAGGAAGTTGAGCGTGCAGT	GAGCCATGACTGTGCGCATGTGTACTTCAGC	2820
Db	3648	TTGCTTGAGCCCAAGGAAGTTGAGCGTGCAGT	GAGCCATGACTGTGCGCATGTGTACTTCAGC	3707
Qy	2821	CTAGTGACAGAGCAAGACCCCTGTCCCTGAC	CCCCCTGAAAAAGAGAGATTAAGT	2880
Db	3708	CTAGTGACAGAGCAAGACCCCTGTCCCTGAC	CCCCCTGAAAAAGAGAGATTAAGT	3767
Qy	2881	TGACTTTGTCTTTATTTTAAATTTTATTTG	CGCCCTGAGCAGTGGGTAATTTGGCAATGCCAT	2940
Db	3768	TGACTTTGTCTTTATTTTAAATTTTATTTG	CGCCCTGAGCAGTGGGTAATTTGGCAATGCCAT	3827
Qy	2941	TTCTGAGATGGTGAAGCCAGAGGAAGACAG	CAGTTTGGGGTAATTAAGGATCTGCAATTTG	3000
Db	3828	TTCTGAGATGGTGAAGCCAGAGGAAGACAG	CAGTTTGGGGTAATTAAGGATCTGCAATTT	3886
Qy	3001	GGACATGTTAAGTTTGAGATTCCAGTCCAGG	CTTCCAAAGTGGTCAAGCCATAGGCAATTT	3060
Db	3887	GGACATGTTAAGTTTGAGATTCCAGTCCAGG	CTTCCAAAGTGGTCAAGCCATAGGCAATTT	3946
Qy	3061	CAGTGTAAAGAAATTCAGGACCAAGCGTGGG	CA CGGTGGCTCACCTCTGTATCTCCAGCACT	3120
Db	3947	CAGTGTAAAGAAATTCAGGACCAAGCGTGGG	CA CGGTGGCTCACCTCTGTATCTCCAGCACT	4006
Qy	3121	TTGTGTGCTCAGGCAGGTAATCATTTGAGGT	CAGGATTTTGAGACAGCTTGCCCAACA	3180
Db	4007	TTGTGTGCTCAGGCAGGTAATCATTTGAGGT	CAGGATTTTGAGACAGCTTGCCCAACA	4066











Qy	2341	ACAGT	GATCTGT	CACAGG	CTTTTAA	AAGATTGCTCTGGCTGCTATGTGGAAAGCAGAA	TGG	2400
Db	1981	ACAGT	GATCTGT	CA	CGCTTTTAA	AAGATTGCTCTGGCTGCTATGTGGAAAGCAGAA	TGG	2040
Qy	2401	AAGG	GAGCAACAGT	AAAA	GAGGAGCC	CAGCAGGAGAGTGTTTACACAGTCCAGGCAAG	2460	
Db	2041	AAGG	GAGCAACAGT	AAAA	GAGGAGCC	CAGCAGGAGAGTGTTTACACAGTCCAGGCAAG	2100	
Qy	2461	AGGT	AGTGGAGTGGG	CTGGTGGG	AACAGAAAGG	AGTGCACAAACATTTGCTCTCTGAA	2520	
Db	2101	AGGT	AGTGGAGTGGG	CTGGTGGG	AACAGAAAGG	AGTGCACAAACATTTGCTCTCTGAA	2160	
Qy	2521	TATAT	CTGAGGAGTGTCTG	AGGATTTCTATGTTGTG	GAGAAAGAGAGAA	TTGG	2580	
Db	2161	TATAT	CTGAGGAGTGTCTG	AGGATTTCTATGTTGTG	GAGAAAGAGAGAA	TTGG	2220	
Qy	2581	CTGG	GTGTAGTGTCTATG	CCAGGAGG	CCCAAGGAGACGATTTCTTGAGTCTCAGGA	2640		
Db	2221	CTGG	GTGTAGTGTCTATG	CCAGGAGG	CCCAAGGAGACGATTTCTTGAGTCTCAGGA	2280		
Qy	2641	GTTCA	GACGACGCTGGG	CAACACAGCAAA	CCCCCTTCTCTACAAAAATACAAAAATTA	2700		
Db	2281	GTTCA	GACGACGCTGGG	CAACACAGCAAA	CCCCCTTCTCTACAAAAATACAAAAATTA	2340		
Qy	2701	GCTGG	GTGTGGCATGCACCTGT	GATCCTAGTACTTCGGAGGCTGAGGTGAGG	TTA	2760		
Db	2341	GCTGG	GTGTGGCATGCACCTGT	GATCCTAGTACTTCGGAGGCTGAGGTGAGG	TTA	2400		
Qy	2761	TTGCT	TGAGGCCAGGAA	TTGAGGCTGCAGT	GAGCCATGACTGTGCCACCTGTACTTCCAGC	2820		
Db	2401	TTGCT	TGAGGCCAGGAA	TTGAGGCTGCAGT	GAGCCATGACTGTGCCACCTGTACTTCCAGC	2460		
Qy	2821	CTAG	TGACAGAGCAAGCCCTGT	CCCCCTGACCCCTGAAAAGAGAGAGTTAAAGT	2880			
Db	2461	CTAG	TGACAGAGCAAGCCCTGT	CCCCCTGACCCCTGAAAAGAGAGAGTTAAAGT	2520			
Qy	2881	TGAC	TTTGTCTTTTATTTT	TAATTTATTTGTCCTGACGAGTGGGTAA	TTGGCAATGCCAT	2940		
Db	2521	TGAC	TTTGTCTTTTATTTT	TAATTTATTTGTCCTGACGAGTGGGTAA	TTGGCAATGCCAT	2580		
Qy	2941	TTCT	GAGATGGTGAAG	CAGAGGAAAGACAGT	TTTGGGGTAAATCAAGGATCTGCATTTG	3000		
Db	2581	TTCT	GAGATGGTGAAG	CAGAGGAAAGACAGT	TTTGGGGTAAATCAAGGATCTGCATTTG	2640		
Qy	3001	GGAC	ATGTTAAGTTTGAGT	TCACGT	CAGGCTCCAAAGTGGTGAGGCCACATAGGCAGTT	3060		
Db	2641	GGAC	ATGTTAAGTTTGAGT	TCACGT	CAGGCTCCAAAGTGGTGAGGCCACATAGGCAGTT	2700		
Qy	3061	CAGT	GTAAAGAAATTCAGG	ACCAAGGCTGGG	CACCGTGGCTCACCTCTGTATCCAGC	3120		
Db	2701	CAGT	GTAAAGAAATTCAGG	ACCAAGGCTGGG	CACCGTGGCTCACCTCTGTATCCAGC	2760		
Qy	3121	TTGG	TGGCTGAGG	CAGGTAGATCATTTGAGGT	CAGGAGTTTGAGACAAGGCTTGCCCAACA	3180		
Db	2761	TTGG	TGGCTGAGG	CAGGTAGATCATTTGAGGT	CAGGAGTTTGAGACAAGGCTTGCCCAACA	2820		
Qy	3181	TGGT	GAAACCCCATGTCT	ACTAAAAATACAAAAAT	TAGCCTGGTGTGGTGGCGCAGCCCT	3240		
Db	2821	TGGT	GAAACCCCATGTCT	ACTAAAAATACAAAAAT	TAGCCTGGTGTGGTGGCGCAGCCCT	2880		
Qy	3241	ATAG	TCCACGTTTTT	CAGGAGGCTTAGGT	AGGAGAAATCCCTTCGACCCAGGAGGTGCAGG	3300		
Db	2881	ATAG	TCCACGTTTTT	CAGGAGGCTTAGGT	AGGAGAAATCCCTTCGACCCAGGAGGTGCAGG	2940		
Qy	3301	TTG	CAGT	GTGAGTGTGTG	CCACTGTGCACTCCAGCCTGGGTGATAGAGTGA	3360		
Db	2941	TTG	CAGT	GTGAGTGTGTG	CCACTGTGCACTCCAGCCTGGGTGATAGAGTGA	3000		
Qy	3361	CTCA	AAAAA	AAAAA	AAAAA	AAAAA	CTGAAGGAATTTATCTCAGGATTTGGG	3420
Db	3001	CTCA	AAAAA	AAAAA	AAAAA	AAAAA	CTGAAGGAATTTATCTCAGGATTTGGG	3060

QY	3421	TCTAAATTTGCCCTGAGCACCAACCTCCTGAGTTGCTAACTACCATGGCTAGACACACCTTTAAC	3480
DB	3061	TCTAAATTTGCCCTGAGCACCAACCTCCTGAGTTGCTAACTACCATGGCTAGACACACCTTTAAC	3120
QY	3481	ATTTTCTTAGAATCCACACAGCTTTTAGTGGAGTCTGTCTAACTCATGAGTATTGGAAATAGGAT	3540
DB	3121	ATTTTCTTAGAATCCACACAGCTTTTAGTGGAGTCTGTCTAACTCATGAGTATTGGAAATAGGAT	3180
QY	3541	CTGGGGCAGTGGAGGGGTGGCACCCAGTGTGGCAGAGAAAAAGCACACAAGGAAAGAGC	3600
DB	3181	CTGGGGCAGTGGAGGGGTGGCACCCAGTGTGGCAGAGAAAAAGCACACAAGGAAAGAGC	3240
QY	3601	ACCAGAGACTGTATATGGAAAGAAAGACAGGACTGCACTCACCCCTTCACAAAATAGGGA	3660
DB	3241	ACCAGAGACTGTATATGGAAAGAAAGACAGGACTGCACTCACCCCTTCACAAAATAGGGA	3300
QY	3661	CCAGACACAGCTGATGTATGAGTTGATGAGGTGTGGAGGCTCAACATCCCTGCTCCC	3720
DB	3301	CCAGACACAGCTGATGTATGAGTTGATGAGGTGTGGAGGCTCAACATCCCTGCTCCC	3360
QY	3721	CTCCTACTACACATGGTTAAGGCGCTGTGTCTGTCTCTCCAGGTTCACTCTCTGCACTA	3780
DB	3361	CTCCTACTACACATGGTTAAGGCGCTGTGTCTGTCTCTCCAGGTTCACTCTCTGCACTA	3420
QY	3781	CCTCTTCATGGGTGCTCAGACAGGACCTTTGGTCTTTTCTGTTTGAAGCTTTGGGCTA	3840
DB	3421	CCTCTTCATGGGTGCTCAGACAGGACCTTTGGTCTTTTCTGTTTGAAGCTTTGGGCTA	3480
QY	3841	CGTGGATGACAGCTGTTTCTGTGTTCTATGATCATGAGAGTGCAGGTCGCGGTGGAGCCCGAAC	3900
DB	3481	CGTGGATGACAGCTGTTTCTGTGTTCTATGATCATGAGAGTGCAGGTCGCGGTGGAGCCCGAAC	3540
QY	3901	TCCATGGGTTTCCAGTAGAAATTTCAAGCCACAGATGTGGCTGCAGCTCAGAGTCAGAGTCTGAA	3960
DB	3541	TCCATGGGTTTCCAGTAGAAATTTCAAGCCACAGATGTGGCTGCAGCTCAGAGTCAGAGTCTGAA	3600
QY	3961	AGGTTGGGATCAATGTTTCACTGTTGACTTCTGGAATAATGGAAAAATCAACAACACAG	4020
DB	3601	AGGTTGGGATCAATGTTTCACTGTTGACTTCTGGAATAATGGAAAAATCAACAACACAG	3660
QY	4021	CAAGGTTATGTGAGAGGGGGCTCACTTCTGAGGTTGTGAGAGCTTTTCACTCTTTTC	4080
DB	3661	CAAGGTTATGTGAGAGGGGGCTCACTTCTGAGGTTGTGAGAGCTTTTCACTCTTTTC	3720
QY	4081	ATGCATCTTCAAGGAAACAGCTCGAAAGTCTGAGGTCTTGTGGAGCAGGGAAGAGGGAAG	4140
DB	3721	ATGCATCTTCAAGGAAACAGCTCGAAAGTCTGAGGTCTTGTGGAGCAGGGAAGAGGGAAG	3780
QY	4141	GAATTTGCTTCTTGAGATCAATTTGGTCTTTGGGATGGTGGAAATAGGACCTATTCTTT	4200
DB	3781	GAATTTGCTTCTTGAGATCAATTTGGTCTTTGGGATGGTGGAAATAGGACCTATTCTTT	3840
QY	4201	TGGTTGCAGTTAACAGGCTGGGGATTTTTCAGAGTCCCAACACCTTCAGGTCATCTCTG	4260
DB	3841	TGGTTGCAGTTAACAGGCTGGGGATTTTTCAGAGTCCCAACACCTTCAGGTCATCTCTG	3900
QY	4261	GGCTGTGAAATCGAAGAAACACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG	4320
DB	3901	GGCTGTGAAATCGAAGAAACACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG	3960
QY	4321	CAGSACCACTTGAATTTCTGCCCTGACACACTGAGTGGAGAGCAGCAGAACCCAGGGCC	4380
DB	3961	CAGSACCACTTGAATTTCTGCCCTGACACACTGAGTGGAGAGCAGCAGAACCCAGGGCC	4020
QY	4381	TGGCCCAACAGCTGAGNTGGGAAAGGCAACAAGTTGGGCTCAGGACAGAACAGGGGCTAC	4440
DB	4021	TGGCCCAACAGCTGAGNTGGGAAAGGCAACAAGTTGGGCTCAGGACAGAACAGGGGCTAC	4080
QY	4441	CTGGAGAGGCACTGCCCTGACACAGCTGCAGAGTGTCTGAGCTGGGAGAGGTGTTTG	4500
DB	4081	CTGGAGAGGCACTGCCCTGACACAGCTGCAGAGTGTCTGAGCTGGGAGAGGTGTTTG	4140
QY	4501	GACCAAACAGGATGTGGAAAAACACTTCTGCTGCCCTACTACTCTAGTGGCAGAGTGGAG	4560



Db	4141	GACCAACAGGATAGTGGTGGAAACACACTTCTGCCCTTACTCTAGTGGCAGAGTGGAGG	4200	
Qy	4561	AGGTTGCAGGGCACGGAATCCCTGGTGGAGTTTCAGAGGTGGCTGAGCTGTGTGCCTC	4620	
Db	4201	AGGTTGCAGGGCACGGAATCCCTGGTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC	4260	
Qy	4621	TCCAAAATTCGGGAAGGGAATTTCTCAATCCCTAGAGTCTTACCTTTATAATTGAGATGTA	4680	
Db	4261	TCCAAAATTCGGGAAGGGAATTTCTCAATCCCTAGAGTCTTACCTTTATAATTGAGATGTA	4320	
Qy	4681	TCAGACAGCCACAAGTCAATGGGTAAATTTCTTTCTCCATGCATATGCTCAGAAGGAA	4740	
Db	4321	TGAGACAGCCACAAGTCAATGGGTAAATTTCTTTCTCCATGCATATGCTCAGAAGGAA	4380	
Qy	4741	GTGTCTATGGCCCTTGCTTTTATTTAAACCAATAATCTTTTGATATATTTATACCTGTAA	4800	
Db	4381	GTGTCTATGGCCCTTGCTTTTATTTAAACCAATAATCTTTTGATATATTTATACCTGTAA	4440	
Qy	4801	AAATTCAGAAATGTCAAGCCCGGGCACGGTGGCTCACCCCTGTAAATCCAGCAGCTTTGGG	4860	
Db	4441	AAATTCAGAAATGTCAAGCCCGGGCACGGTGGCTCACCCCTGTAAATCCAGCAGCTTTGGG	4500	
Qy	4861	AGGCCGAGCGGGTGG- - -TCACAAGGTCAGGAGTTTGAGACCGCCTGACCAACATGCT	4917	
Db	4501	AGGCCGAGCGGCGAGACATCACTGAGGTCAGGAGTTTGAGACCGCCTGACCAACATGCT	4560	
Qy	4918	GAACCCCGTCTCTAAAAAATAACAAAAATTAGCTGGTCACAGTCATGCGCACCTGTAGTC	4977	
Db	4561	GAACCCCGTCTCTAAAAAATAACAAAAATTAGCTGGTCACAGTCATGCGCACCTGTAGTC	4620	
Qy	4978	CCAGCTAATTTGGAAGCTGAGGC	5000	
Db	4621	CCAGCTACTCGGGAGGCTGAGGC	4643	
RESULT 11				
US-10-311-455-2115				
; Sequence 2115, Application US/10311455				
; Publication No. US20030143606A1				
; GENERAL INFORMATION:				
; APPLICANT: OLEK, Alexander				
; APPLICANT: PIEPENBROCK, Christian				
; APPLICANT: BERLIN, Kurt				
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ				
; FILE OF INVENTION: cytosine methylation				
; FILE REFERENCE: 5013.1014				
; CURRENT APPLICATION NUMBER: US/10/311,455				
; PRIORITY FILING DATE: 2002-12-16				
; PRIOR APPLICATION NUMBER: PCT/EP01/07537				
; PRIOR FILING DATE: 2001-07-02				
; PRIOR APPLICATION NUMBER: DE 10032529.7				
; PRIOR FILING DATE: 2000-06-30				
; PRIOR APPLICATION NUMBER: DE 10043826.1				
; PRIOR FILING DATE: 2000-09-01				
; NUMBER OF SEQ ID NOS: 2424				
; SEQ ID NO 2115				
; LENGTH: 8622				
; TYPE: DNA				
; ORGANISM: Artificial Sequence				
; FEATURE:				
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)				
US-10-311-455-2115				
Query Match 51.1%; Score 2556.4; DB 15; Length 8622;				
Best Local Similarity 80.1%; Pred. No. 0;				
Matches 3015; Conservative 0; Mismatches 746; Indels 1; Gaps 1;				
Qy	1	TCTAAGGTTGAGATAAAATTTTAAATGTATGATGAATTTTGAATAATCATATAATTTA	60	
Db	4862	TTTAAAGGTTGAGATAAAATTTTAAATGTATGATGAATTTTGAATAATCATATAATTTA	4921	
Qy	61	AATAATCTAAAGTTCAGATCAGAACATTTGGAGGCTACTTTTCCCAATCAACAACCCCT	120	











2501 TTTTCACTAAACATAAAAAATAAAAACTAAATAATAGCTTTATTTTACTAAAAATAAAT 2442  
1321 GGAAATTCAGATATATAAATCTTTTTCAGGTTACAAAGAACATAAATAATCTGGTTTCG 1380  
2441 ABAATTCAAATTAATATACTTTTCAAATTACAAAACATANAATAATCTAATTTTCTA 2382  
1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTGACAGTAGTTTGGCCCTGTAG 1440  
2381 ATATTATTTCAAAATACCTACAACTACTTCTAATCTTAATTAACAATAATTTTACCCTATAA 2322  
1441 TGTAGCACAGTGTCTGTGGGTACACGCGCGCTCAGACACAGCATTGAGTTTGGTA 1500  
2321 TATAACACAATAATTTCTAATAATCACAGCGCGCTCAACACACACACTTTTAAATTTTAAATA 2262  
1501 CTACGTGTATCCACATTTTACACATGACCAAGATGAGGATGCGCGCTGCTCCTCG 1560  
2261 CTACGTATATCCATTTTACACATGACCAAAATAAACAATACACAGCCTACTTCTTAA 2202  
1561 CAAATTTATTCATGTTTCACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTTCATAGC 1620  
2201 CAAATTTATTCATTAATAACATACTTAACTTAAATAAATAAATAAATAAATAAATAAATAA 2142  
1621 TATGATTTTAAACATCACCTGCTTATGAGTTGAATAATAAATAAATAAATAAATAAATAA 1680  
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1681 AATATTTCTTATTTTCAAGTGTAAATGATGCTCCAGCCATGTTGTCACCTGTTCAAGCCC 1740  
2081 AATATTTCTTATTTTCAAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2022  
1741 CAAGGAGAGAGCAGGGAACCAAGTCTTTTACCCTTTGATATTTTGCATTTAGTGGGAGA 1800  
2021 CAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1962  
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1781 TTAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1722  
2041 CGCGGTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATGCTAGCAGTATCCTGT 2100  
1721 CGAGTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1662  
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1661 CCTCCCTACTACTAAATACTAATAAACAATCTCCCGCAATCTTAACAACCAAAATATCTCT 1602  
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1601 AAACTTTTACCACATATCACTAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1542  
2221 AATAACAAGTAGTCTGGGAGTAGGCGCAAGAGTAGGTAAATGGGCTCAGAGAGGA 2280  
1541 AATAACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1482  
2281 GCCAATAAAGGTTGTGAGGCGCTGTAGGCTGTGGTGTGAATTTCTAGCCAAAGGTA 2340  
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1361 AAAAAACAACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1302  
2461 AGGTAGTGGAGTGGGCTGGGGAACAGAAAAAGGAGTGACAAACCAATTTGTCTCTGAA 2520  
1301 AATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1242  
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2641 GTTCAAGACCAAGCTGGGCAACACAGCAAAACCCCTTCTTACAAAAATACAAAAATTA 2700  
1121 ATTCAAAACCAACCTTAAACCAACCAAAACCCCTTCTTACAAAAATACAAAAATTA 1062  
2701 GCTGGGTGTGGGATGACCTGTGATCTAGTACTCTGGGAGGCTGAGGTGGAGGTA 2760  
1061 ACTAAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1002  
2761 TTGCTTGGAGCCAGGAAGTTGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2820  
1001 TTACTTAAACCCAAAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 942  
2821 CTAGGTGACAGAGCAAGCCCTGTCTCCCTGACCCCTTGAAGAGAGAGAGAGAGAGAGT 2880  
941 CTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 882  
2881 TGACTTTGTTCTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 2940  
881 TAACTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 822  
2941 TTTCTAGATGTTGAAGGAGT 3000  
821 TTTCTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 763  
3001 GGACATGTTTAAAGTTTGTAGATTTCCAGTCCAGGCTTCCAGTGGTGAGGCCACATAGGAGT 3060  
762 AAACATATTTAAATTTTAAATTTTCAATCAAACTTCCAAATAATAAATAAATAAATAAATAA 703  
3061 CAGTGTAGAAATTTAGGACCAAGGCTGGGAGCGGTGAGTCTTCTGTATATCCAGCACT 3120  
702 CAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 643  
3121 TTTGGTGGCTGAGGAGGAGTATGATTTTGGAGGTCAGGAGTTTGGAGACAGCTTTGGCCAA 3180  
642 TTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 583  
3181 TGGTGAACCCCATGCTCTACTAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3240  
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3241 ATAGTCCAGGTTTTCAGGAGGCTTAGGTAGAGAAATCCCTTGAACCCAGGAGGTGAGG 3300  
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462 TTACAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 403  
3361 CTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3420  
402 CTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 343  
3421 TCTAATTTGCCGTGAGCAGCAACTCCTCAGTTTCACTACCAATGAGGTAGACACACCTTTAAC 3480  
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/ PRIOR APPLICATION NUMBER: 60/218,290
/ PRIOR FILING DATE: 2000-07-14
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 4031
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3112
/ LENGTH: 5749
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1222)
/ OTHER INFORMATION: n equals a.t.g, or c
US-10-242-515-3112

Query Match      20.0%; Score 998.4; DB 17; Length 5749;
Best Local Similarity 99.9%; Pred. No. 8.1e-259;
Matches 999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4001 ATGGAATAATCACAAACACACAGAGGATGTGTGAGAGGGGCGCTCACCTTCTCTGAGGTTG 4060
DB 1 ATGGAATAATCACAAACACACAGAGGATGTGTGAGAGGGGCGCTCACCTTCTCTGAGGTTG 60

QY 4061 TCAGAGCTTTTCATCTTTTCATGTCATCTTGAAGAAACAGCTGGAAGTCTGAGGTTCTGT 4120
DB 61 TCAGAGCTTTTCATCTTTTCATGTCATCTTGAAGAAACAGCTGGAAGTCTGAGGTTCTGT 120

QY 4121 GGGAGCAGGAGAGAGGAGGATTTGCTTCTGAGATCATTTGCTTCTGAGGATGTTG 4180
DB 121 GGGAGCAGGAGAGAGGAGGATTTGCTTCTGAGATCATTTGCTTCTGAGGATGTTG 180

QY 4181 GAAATAGGAGCATTATCTTTTGGTTGTCAGTTAAACAGGCTGGGATTTTTCAGAGTCCC 4240
DB 181 GAAATAGGAGCATTATCTTTTGGTTGTCAGTTAAACAGGCTGGGATTTTTCAGAGTCCC 240

QY 4241 ACACCTCGAGGTCATCTTGGGCTGTGAAATGCAAGAACACAGTACCGAGGGCTACT 4300
DB 241 ACACCTCGAGGTCATCTTGGGCTGTGAAATGCAAGAACACAGTACCGAGGGCTACT 300

QY 4301 GGAAGTACGGGTATGATGGCAGGACCTTGAATTTCTGCTTGCCTGCACACTGGATTGA 4360
DB 301 GGAAGTACGGGTATGATGGCAGGACCTTGAATTTCTGCTTGCCTGCACACTGGATTGA 360

QY 4361 GAGCAGCAGAACCCAGGGGCTTGCCCCACCAAGCTGGAGTGGGAAGGCAAGATTTCGGG 4420
DB 361 GAGCAGCAGAACCCAGGGGCTTGCCCCACCAAGCTGGAGTGGGAAGGCAAGATTTCGGG 420

QY 4421 CCAGGCAGAACAGGGCTTACCTGGAGAGGACTGCCCCGCACAGCTGCAGAGTTGCTGG 4480
DB 421 CCAGGCAGAACAGGGCTTACCTGGAGAGGACTGCCCCGCACAGCTGCAGAGTTGCTGG 480

QY 4481 AGCTGGGGAGAGTGTGTTGGACCAACAGGATGTGTGAAACACACTTCTGCCCTATA 4540
DB 481 AGCTGGGGAGAGTGTGTTGGACCAACAGGATGTGTGAAACACACTTCTGCCCTATA 540

QY 4541 CTCTAGTGCAGAGTGGAGAGGTTGTCAGGGCAGGAATCCCTGGTTGGAGTTTCAGAGG 4600
DB 541 CTCTAGTGCAGAGTGGAGAGGTTGTCAGGGCAGGAATCCCTGGTTGGAGTTTCAGAGG 600

QY 4601 TGGCTGAGGCTGTGTCCTTCCAAATTCCTGGGAAGGACTTCTCAATCTTAGAGTCTC 4660
DB 601 TGGCTGAGGCTGTGTCCTTCCAAATTCCTGGGAAGGACTTCTCAATCTTAGAGTCTC 660

QY 4661 TACCTTATATTCAGATGTATGAGCAGGCAACAGTCATGGGTTAAATTTCTTTCTCCA 4720
DB 661 TACCTTATATTCAGATGTATGAGCAGGCAACAGTCATGGGTTAAATTTCTTTCTCCA 720

QY 4721 TGCATATGGCTCAAAGGGAAGTGTCTATGGCCCTTGTCTTTTATTTAAACCAATATCTTT 4780
DB 721 TGCATATGGCTCAAAGGGAAGTGTCTATGGCCCTTGTCTTTTATTTAAACCAATATCTTT 780

QY 4781 TGTATATTTATCTGTTTAAAAAATTCAGAAATGTCAAGSCCGGCAACGCTGGCTCACCCC 4840
DB TGTATATTTATCTGTTTAAAAAATTCAGAAATGTCAAGSCCGGCAACGCTGGCTCACCCC 4840
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DB 781 TGTATATTTATCTGTTTAAAAAATTCAGAAATGTCAAGSCCGGCAACGCTGGCTCACCCC 840
QY 4841 TGTATATTTATCTGTTTAAAAAATTCAGAAATGTCAAGSCCGGCAACGCTGGCTCACCCC 4900
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QY 4901 AGCCTGACCAACATGTTGAAACCCGCTCTCTTAAAAAATACAAAAATTAGCTGCTCACAGT 4960
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DB 961 CATGGCACCTGTAGTCCAGCTAATTTGGAAGCTGAGGC 1000

RESULT 15
US-10-029-386-10129
; Sequence 10129, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10129
; LENGTH: 500
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR6.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
; OTHER INFORMATION: NT HIT: U91328.1, EVALUATE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q30201, EVALUATE 1.00e-52
; OTHER INFORMATION: EST_HUMAN HIT: BG747345.1, EVALUATE 0.00e+00
US-10-029-386-10129

Query Match      10.0%; Score 500; DB 16; Length 500;
Best Local Similarity 100.0%; Pred. No. 2.2e-124;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4129 GGAAGAGGGAAGGAATTTGCTTCTGAGATCATTTTGGTCTTGGGATGTTGGAATAGG 4188
DB 1 GGAAGAGGGAAGGAATTTGCTTCTGAGATCATTTTGGTCTTGGGATGTTGGAATAGG 60

QY 4189 GACCTATTCTTTTGGTTGTCAGTTAAACAAGGCTGGGGATTTTTCAGAGTCCACACCCCTG 4248
DB 61 GACCTATTCTTTTGGTTGTCAGTTAAACAAGGCTGGGGATTTTTCAGAGTCCACACCCCTG 120

QY 4249 CAGGTATCTTGGGCTGTGAAATGCAAGAACACAGTACCGAGGCTACTTGGAAAGTAC 4308
DB 121 CAGGTATCTTGGGCTGTGAAATGCAAGAACACAGTACCGAGGCTACTTGGAAAGTAC 180

QY 4309 GGGTATGATGGCAGGACACCTTGAATTTCTGCCCTGACACACTGATTTGGAGAGCAGCA 4368
DB 181 GGGTATGATGGCAGGACACCTTGAATTTCTGCCCTGACACACTGATTTGGAGAGCAGCA 240

QY 4369 GAACCCAGGCGCTTGGCCCAACCAAGCTGGAGTGGGAAAGGCAACAAGTTGGGCCAGGCGAG 4428
DB 241 GAACCCAGGCGCTTGGCCCAACCAAGCTGGAGTGGGAAAGGCAACAAGTTGGGCCAGGCGAG 300

QY 4429 AACAGGCGCTTACCTGGAGAGGAGCTGCCCTGCAAGCTGCAGAGTTCGTGGAGCTGGGG 4488
DB 301 AACAGGCGCTTACCTGGAGAGGAGCTGCCCTGCAAGCTGCAGAGTTCGTGGAGCTGGGG 360
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Qy	4489	AGAGGTGTTTGGACCAACAAGGTATGGTGGAAACACACACTTCTGCCCCCTATACTCTAGTG	4548
Db	361		420
Qy	4549	GCAGAGTGGAGGAGGTTGCAGGGCCACGGAAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAG	4608
Db	421		480
Qy	4609	GCTGTGTCCTCTCCAAATT	4628
Db	481		500

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Job time : 2901.98 secs